* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1 Web Page for STN Seminar Schedule - N. America
NEWS 2 APR 04 STN AnaVist, Version 1, to be discontinued
NEWS 3 APR 15 WPIDS, WPINDEX, and WPIX enhanced with new predefined hit display formats
NEWS 4 APR 28 EMBASE Controlled Term thesaurus enhanced
NEWS 5 APR 28 IMSRESEARCH reloaded with enhancements
NEWS 6 MAY 30 INPAFAMDB now available on STN for patent family searching
NEWS 7 MAY 30 DGENE, PCTGEN, and USGENE enhanced with new homology sequence search option
NEWS 8 JUN 06 EPFULL enhanced with 260,000 English abstracts
NEWS 9 JUN 06 KOREAPAT updated with 41,000 documents
NEWS 10 JUN 13 USPATFULL and USPAT2 updated with 11-character patent numbers for U.S. applications
NEWS 11 JUN 19 CAS REGISTRY includes selected substances from web-based collections
NEWS 12 JUN 25 CA/CAplus and USPAT databases updated with IPC reclassification data
NEWS 13 JUN 30 AEROSPACE enhanced with more than 1 million U.S. patent records
NEWS 14 JUN 30 EMBASE, EMBAL, and LEMBASE updated with additional options to display authors and affiliated organizations
NEWS 15 JUN 30 STN on the Web enhanced with new STN AnaVist Assistant and BLAST plug-in
NEWS 16 JUN 30 STN AnaVist enhanced with database content from EPFULL
NEWS 17 JUL 28 CA/CAplus patent coverage enhanced
NEWS 18 JUL 28 EPFULL enhanced with additional legal status information from the epoline Register
NEWS 19 JUL 28 IFICDB, IFIPAT, and IFIUDB reloaded with enhancements
NEWS 20 JUL 28 STN Viewer performance improved
NEWS 21 AUG 01 INPADOCDB and INPAFAMDB coverage enhanced
NEWS 22 AUG 13 CA/CAplus enhanced with printed Chemical Abstracts page images from 1967-1998
NEWS 23 AUG 15 CAOLD to be discontinued on December 31, 2008
NEWS 24 AUG 15 CAplus currency for Korean patents enhanced
NEWS 25 AUG 25 CA/CAplus, CASREACT, and IFI and USPAT databases enhanced for more flexible patent number searching
NEWS 26 AUG 27 CAS definition of basic patents expanded to ensure comprehensive access to substance and sequence information

NEWS EXPRESS JUNE 27 08 CURRENT WINDOWS VERSION IS V8.3, AND CURRENT DISCOVER FILE IS DATED 23 JUNE 2008.

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NEWS LOGIN Welcome Banner and News Items
NEWS IPC8 For general information regarding STN implementation of IPC 8

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FILE 'HOME' ENTERED AT 15:16:47 ON 06 SEP 2008

=> file caplus
COST IN U.S. DOLLARS SINCE FILE
TOTAL ENTRY SESSION
FULL ESTIMATED COST 0.21 0.21

FILE 'CAPLUS' ENTERED AT 15:17:05 ON 06 SEP 2008
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 6 Sep 2008 VOL 149 ISS 11
FILE LAST UPDATED: 5 Sep 2008 (20080905/ED)

Caplus now includes complete International Patent Classification (IPC)
reclassification data for the second quarter of 2008.

Effective October 17, 2005, revised CAS Information Use Policies apply.
They are available for your review at:

http://www.cas.org/legal/infopolicy.html

=> s (array? or microarray?)/bi,ab 193951 ARRAY?/BI
180462 ARRAY?/AB 64134 MICROARRAY?/BI
38186 MICROARRAY?/AB
L1 243828 (ARRAY? OR MICROARRAY?)/BI,AB

=> s mitochondi?/bi,ab 12 MITOCHONDI?/BI
4 MITOCHONDI?/AB
L2 12 MITOCHONDI?/BI,AB

=> s mitochondri?/bi,ab 181246 MITOCHONDRI?/BI
163776 MITOCHONDRI?/AB
L3 181246 MITOCHONDRI?/BI,AB

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=> s l1 and l3
L4        2169 L1 AND L3

=> l4 not 2008/py
L4 IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the
system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l4 not 2008/py   1084128 2008/PY
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=> s l5 not 2007/py   1641226 2007/PY
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=> s l6 not 2006/py   1548055 2006/PY
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=> s l7 not 2005/py   1408583 2005/PY
L8         930 L7 NOT 2005/PY

=> s l8 not 2004/py   1332063 2004/PY
L9         708 L8 NOT 2004/PY

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L7         1201 S L6 NOT 2006/PY
L8          930 S L7 NOT 2005/PY
L9          708 S L8 NOT 2004/PY

=> s l9 and (dna# or cdna# or rna#)/bi ab
MISSING OPERATOR

=> s l9 and (dna# or cdna# or rna#)/bi,ab    919421 DNA#/BI
697798 DNA#/AB                224458 CDNA#/BI
172323 CDNA#/AB                366476 RNA#/BI
278497 RNA#/AB
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L9          708 S L8 NOT 2004/PY
L10         438 S L9 AND (DNA# OR CDNA# OR RNA#)/BI,AB

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0 (CAENORABDIS)/AB
L11           0 (CAENORABDIS)/BI,AB

=> s ceanorabdis/bi,ab          0 CEANORABDIS/BI
0 CEANORABDIS/AB
L12           0 CEANORABDIS/BI,AB

=> s caenorhabdus/bi,ab          0 CAENORHABDUS/BI
0 CAENORHABDUS/AB
L13           0 CAENORHABDUS/BI,AB

=> s caenorabdus/bi,ab          0 CAENORABDUS/BI
0 CAENORABDUS/AB
L14           0 CAENORABDUS/BI,AB

=> s caenorhabditis/bi,ab      14138 CAENORHABDITIS/BI
9383 CAENORHABDITIS/AB
L15       14138 CAENORHABDITIS/BI,AB

=> s elegans/bi,ab      17793 ELEGANS/BI                  14454
ELEGANS/AB
L16       17793 ELEGANS/BI,AB

=> s nematode#/bi,ab      21945 NEMATODE#/BI
16720 NEMATODE#/AB
L17       21945 NEMATODE#/BI,AB

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L9          708 S L8 NOT 2004/PY
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L12           0 S CEANORABDIS/BI,AB
L13           0 S CAENORHABDUS/BI,AB
L14           0 S CAENORABDUS/BI,AB
L15       14138 S CAENORHABDITIS/BI,AB
L16       17793 S ELEGANS/BI,AB
L17       21945 S NEMATODE#/BI,AB
L18       33916 S L15 OR L16 OR L17

=> s l10 and l18
L19           4 L10 AND L18

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L6         1513 S L5 NOT 2007/PY
L7         1201 S L6 NOT 2006/PY
L8          930 S L7 NOT 2005/PY
L9          708 S L8 NOT 2004/PY
L10         438 S L9 AND (DNA# OR CDNA# OR RNA#)/BI,AB
L11           0 S (CAENORABDIS)/BI,AB
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L13 0 S CAENORHABDUS/BI,AB
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L15 14138 S CAENORHABDITIS/BI,AB
L16 17793 S ELEGANS/BI,AB
L17 21945 S NEMATODE#/BI,AB
L18 33916 S L15 OR L16 OR L17
L19 4 S L10 AND L18

=> d l19 1-4 bib ab

L19 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:159403 CAPLUS <<LOGINID::20080906>>
DN 136:178994
TI Protein and ***cDNA*** of novel human ***mitochondria*** -associated ribosomal protein L4 sequence homolog and uses in therapy
IN Mao, Yumin; Xie, Yi
PA Shanghai Shengyuan Gene Development Co., Ltd., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 24 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
---------- ---- -------- ---------- --------
PI CN 1310185 A 20010829 CN 2000-111730 20000224
PRAI CN 2000-111730 20000224
AB The invention provides protein and ***cDNA*** sequences of one new human ***mitochondria*** -assocd. 60S ribosomal protein L4 sequence homolog cloned from human embryonic brain by RT-PCR with specific primers. The invention related the methods of using the protein and ***DNA*** for treatment of various diseases, such as ***mitochondrial*** myopathy, neurodegenerative disorder, immune disorder, and malignant tumors. The invention provides methods, expression vectors, host cells for recombinant prodn. of the protein, and antibody against the protein.

L19 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:797661 CAPLUS <<LOGINID::20080906>>
DN 137:58401
TI Rapid decrease of ***RNA*** level of a novel mouse ***mitochondria*** solute carrier protein (Mscp) gene at 4-5 weeks of age
AU Li, Quan-Zhen; Eckenrode, Sarah; Ruan, Qing-Guo; Wang, Cong-Yi; Shi, Jing-Da; McIndoe, Richard A.; She, Jin-Xiong
CS Department of Pathology, Immunology and Laboratory Medicine, Center for Mammalian Genetics, and Diabetes Center of Excellence, University of Florida, College of Medicine, Gainesville, FL, 32610, USA
SO Mammalian Genome (2001), 12(11), 830-836 CODEN: MAMGEC; ISSN: 0938-8990
PB Springer-Verlag New York Inc.
DT Journal
LA English
AB We cloned a novel mouse gene that encodes a protein with homol. to the ***mitochondria*** solute carrier proteins (Mscp). The major full-length Mscp transcript contains 4112 bp of ***cDNA*** and a deduced protein of 338 amino acids. The Mscp protein shares 50%, 40%, and 39% sequence identity with the C. ***elegans*** hypothetical protein T26089 and the yeast ***mitochondria*** carrier proteins MRS3 and MRS4, resp. It also showed homol. with the uncoupling proteins (UCP1, UCP2, and UCP3; 22%, 24%, and 29% identity, resp.). The protein has six transmembrane domains and three ***mitochondria*** energy-transfer protein signature motifs, which are conserved among all the members of ***mitochondria*** carrier protein family. Northern anal. indicated that the Mscp gene is highly expressed in the spleen. Using ***cDNA*** ***microarray*** and Northern anal., we have shown a significant decrease of the splenic Mscp mRNA levels around 4-5 wk of age in several mouse strains including C57BL/6J, nonobese diabetic (NOD), and several NOD-congenic mice. These results suggest that the Mscp gene is decreased during splenic lymphocyte maturation in these mice.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L19 ANSWER 3 OF 4 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:590343 CAPLUS <<LOGINID::20080906>>
DN 132:232646
TI Changes of gene expression in human astrocytic brain tumors
AU Dmitrenko, V. V.; Shostak, K. O.; Garifulin, O. M.; Zozulya, Yu. A.; Kavsan, V. M.
CS Institute of Molecular Biology and Genetics, National Academy of Sciences of Ukraine, Kiev, 252143, Ukraine
SO Eksperimental'naya Onkologiya (1998), 20(3-4), 191-197 CODEN: EKSODD; ISSN: 0204-3564
PB Institut Eksperimental'noi Patologii, Onkologii i Radiobiologii im. R. E. Kavetskogo NAN Ukrainy
DT Journal
LA English
AB Differential hybridization of high d. grids of ***arrayed*** human fetal brain ***cDNA*** library was used for identification of new tumor markers. Nine clones contg. ***cDNAs*** complementary to the transcripts of differentially expressed genes were selected for further anal. after confirmation of their changed expression in brain astrocytic tumors by Southern hybridization. In this work the authors characterize three clones with ***cDNA*** copies of transcripts overexpressed in glioblastoma multiforme. F0246 mRNA encodes the protein partially homologous to human TRAF6, one of the tumor necrosis factor (TNF) receptor-assocd. factors involved in signal transduction from various members of the TNF receptor superfamily. ***CDNA*** insert of M243 clone is complementary to human ***mitochondrial*** 16S rRNA. The increasing expression level of mt 16S rRNA gene in glioblastoma multiforme and in other types of malignant tumors may serve as a general tumor marker. G2490 ***cDNA*** contains an open reading frame for the protein with a 86% homol. to hypothetical 9.8 kD protein ZK652.3 encoded by chromosome 3 of ***Caenorhabditis*** ***elegans*** . Highly conservative structure of protein in evolutionary distant organisms may testify to the importance of its function.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L19 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:330250 CAPLUS <<LOGINID::20080906>>
DN 127:45927
OREF 127:8655a
TI Animal ***mitochondrial*** ***DNA*** recombination
AU Lunt, David H.; Hyman, Bradley C.
CS Dep. Biology, Univ. California, Riverside, CA, 92521, USA
SO Nature (London) (1997), 387(6630), 247 CODEN: NATUAS; ISSN: 0028-0836

PB Macmillan Magazines
DT Journal
LA English
AB Contrary to the consensus view that genetic recombination does not occur in animal ***mitochondrial*** ***DNA*** (mtDNA), the authors found end-products of recombination in the ***mitochondrial*** genome of the phytonematode, Meloidogyne javanica. Sequences of ***nematode*** mtDNA VNTRs frequently contained deletions in the center of the ***array*** , indicating that genetic recombination might be occurring. Small circular mols. composed of M. javanica mtDNA sequences were detected using PCR and subsequent sequence anal.; these appear to be subgenomic recombination end-products.
RE.CNT 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L2 12 S MITOCHONDI?/BI,AB
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L4 2169 S L1 AND L3
L5 1872 S L4 NOT 2008/PY
L6 1513 S L5 NOT 2007/PY
L7 1201 S L6 NOT 2006/PY
L8 930 S L7 NOT 2005/PY
L9 708 S L8 NOT 2004/PY
L10 438 S L9 AND (DNA# OR CDNA# OR RNA#)/BI,AB
L11 0 S (CAENORABDIS)/BI,AB
L12 0 S CEANORABDIS/BI,AB
L13 0 S CAENORHABDUS/BI,AB
L14 0 S CAENORABDUS/BI,AB
L15 14138 S CAENORHABDITIS/BI,AB
L16 17793 S ELEGANS/BI,AB
L17 21945 S NEMATODE#/BI,AB
L18 33916 S L15 OR L16 OR L17
L19 4 S L10 AND L18

=> s ((array? or microarray?)(5a)mitochondri?)/bi,ab 193951 ARRAY?/BI 180462 ARRAY?/AB 64134 MICROARRAY?/BI 38186 MICROARRAY?/AB 181246 MITOCHONDRI?/BI 163776 MITOCHONDRI?/AB
L20 283 ((ARRAY? OR MICROARRAY?)(5A)MITOCHONDRI?)/BI,AB

=> s ((array? or microarray?)(10a)mitochondri?)/bi,ab 193951 ARRAY?/BI 180462 ARRAY?/AB 64134 MICROARRAY?/BI 38186 MICROARRAY?/AB 181246 MITOCHONDRI?/BI 163776 MITOCHONDRI?/AB
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L22 376 L21 NOT 2008/PY

=> s l22 not 2007/py 1641226 2007/PY
L23 304 L22 NOT 2007/PY

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L24 239 L23 NOT 2006/PY

=> s l24 not 2005/py 1408583 2005/PY
L25 190 L24 NOT 2005/PY

=> s l25 not 2004/py 1332063 2004/PY
L26 151 L25 NOT 2004/PY

=> s l20 not 2008/py 1084128 2008/PY
L27 248 L20 NOT 2008/PY

=> s l27 not 2007/py 1641226 2007/PY
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=> s l28 not 2006/py 1548055 2006/PY
L29 155 L28 NOT 2006/PY

=> s l29 not 2005/py 1408583 2005/PY
L30 119 L29 NOT 2005/PY

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L31 91 L30 NOT 2004/PY

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L19 4 S L10 AND L18
L20 283 S ((ARRAY? OR MICROARRAY?)(5A)MITOCHONDRI?)/BI,AB
L21 423 S ((ARRAY? OR MICROARRAY?)(10A)MITOCHONDRI?)/BI,AB
L22 376 S L21 NOT 2008/PY
L23 304 S L22 NOT 2007/PY
L24 239 S L23 NOT 2006/PY
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L26 151 S L25 NOT 2004/PY
L27 248 S L20 NOT 2008/PY
L28 196 S L27 NOT 2007/PY
L29 155 S L28 NOT 2006/PY
L30 119 S L29 NOT 2005/PY
L31 91 S L30 NOT 2004/PY

=> d l26 1-151 bib ab

L26 ANSWER 1 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2005:613269 CAPLUS <<LOGINID::20080906>>
DN 143:127686
TI Automatable virtual ***array*** screening system for rapid analysis of ***mitochondrial*** DNA polymorphism

AU Campbell, Rowan Stewart
CS Health Science Center, Univ. of North Texas, Fort Worth, TX, USA
SO (2002) 142 pp. Avail.: UMI, Order No. DA3134633 From: Diss. Abstr. Int., B 2004, 65(5), 2236
DT Dissertation
LA English
AB Unavailable

L26 ANSWER 2 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2005:404195 CAPLUS <<LOGINID::20080906>>
DN 143:303494
TI Nuclear genes involved in mitochondria-to-nucleus communication in breast cancer cells
AU Delsite, Robert; Kachhap, Sushant; Anbazhagan, Ramaswamy; Gabrielson, Edward; Singh, Keshav K.
CS Sidney Kimmel Cancer Center, Johns Hopkins School of Medicine, Baltimore, MD, 21231, USA
SO Molecular Cancer (2002), 1, No pp. given CODEN: MCOACG; ISSN: 1476-4598 URL: http://www.molecular-cancer.com/content/pdf/1476-4598-1-6.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Background: The interaction of nuclear and mitochondrial genes is an essential feature in maintenance of normal cellular function. Of 82 structural subunits that make up the oxidative phosphorylation system in the mitochondria, mitochondrial DNA (mtDNA) encodes 13 subunits and rest of the subunits are encoded by nuclear DNA. Mutations in mitochondrial genes encoding the 13 subunits have been reported in a variety of cancers. However, little is known about the nuclear response to impairment of mitochondrial function in human cells. Results: We isolated a Rho0 (devoid of mtDNA) deriv. of a breast cancer cell line. Our study suggests that depletion of mtDNA results in oxidative stress, causing increased lipid peroxidn. in breast cancer cells. Using a cDNA microarray we compared differences in the nuclear gene expression profile between a breast cancer cell line (parental Rho+) and its Rho0 deriv. impaired in mitochondrial function. Expression of several nuclear genes involved in cell signaling, cell architecture, energy metab., cell growth, apoptosis including general transcription factor TFIIH, v-maf, AML1, was induced in Rho0 cells. Expression of several genes was also down-regulated. These include phospholipase C, agouti related protein, PKC gamma, protein tyrosine phosphatase C, phosphodiesterase 1A (cell signaling), PIBFI, cytochrome P 450, (metab.) and cyclin dependent kinase inhibitor p19, and GAP43 (cell growth and differentiation). Conclusions: Mitochondrial impairment in breast cancer cells results in altered expression of nuclear genes involved in signaling cellular architecture, metab., cell growth and differentiation, and apoptosis. These genes may mediate the cross talk between mitochondria and the nucleus.
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 3 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2005:363473 CAPLUS <<LOGINID::20080906>>
DN 143:54591
TI Bioassay of pesticide lindane using yeast-DNA microarray technology
AU Parveen, Meher; Momose, Yuko; Kitagawa, Emiko; Kurita, Sakiko; Kodama, Osamu; Iwahashi, Hitoshi
CS United Graduate School of Agricultural Science, Tokyo University of Agriculture and Technology, Japan
SO Chem-Bio Informatics Journal (2003), 3(1), 12-29 CODEN: CIJHBB; ISSN: 1347-0442 URL: http://www.cbi.or.jp/cbi/CBIj/vol3/3_12-E.pdf
PB Chem-Bio Informatics Society
DT Journal; (online computer file)
LA English
AB The authors analyzed the gene expression pattern of Saccharomyces cerevisiae in response to lindane, a strong toxicant widely used as a pesticide in agriculture and by public health services. CDNA prepns. from untreated cells and from cells treated with lindane were used to screen the DNA microarrays of about 6,000 genes. A total of 288 genes showed >2-fold induction in transcript levels, out of which 112 have not yet been characterized. The functional anal. of most known genes indicates that genes involved with mitochondrial dysfunction, oxidative stress, ionic homeostasis, mitochondrial organization, or biogenesis responded to lindane-mediated stress. In addn., several induced genes were shown to contribute to ER-mediated degrdn. and quality control. However, no significant changes in the transcript levels of ORFs related to DNA damage and repair were obsd. Furthermore, the mRNA levels of some uncharacterized genes are significantly high, and the unveiling of these genes, along with that of known genes, might provide the opportunity to illustrate how yeast responds to environmental perturbation. This anal. will also facilitate the identification of some specific genes that could be used as biomarkers for a toxicity assay of lindane or other similar environmental pollutants.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 4 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2005:46202 CAPLUS <<LOGINID::20080906>>
DN 142:195160
TI Nuclear genes affected in human mitochondrial deficiencies: perspectives from the human genome sequence
AU Santorelli, Filippo M.; Carrozzo, Rosalba
CS Molecular Medicine, IRCCS-Bambino Gesu, Rome, 4-00165, Italy
SO Recent Research Developments in Human Mitochondrial Myopathies (2002), 33-52. Editor(s): Garcia-Trejo, Jose de Jesus. Publisher: Research Signpost, Trivandrum, India. CODEN: 69GJGW; ISBN: 81-7736-139-2
DT Conference; General Review
LA English
AB A review. Disorders of oxidative phosphorylation (OXPHOS) are assocd. with a diverse ***array*** of multisystem diseases often referred to as ***mitochondrial*** encephalomyopathies because of the prominent involvement of the central nervous system and the skeletal muscle. Once believed to be rare, it is now clear that OXPHOS deficiencies are an important cause of a wide range of neuromuscular, cardiac and endocrine disorders, and even some cancers. In children, for instance, a large no. of metabolic encephalomyopathies are due to autosomal recessive defects in OXPHOS genes, usually with severe phenotypes and a fatal outcome. In 1988, optimal use of databases from the National Center for Biotechnol. proved to be important in the identification of the nuclear-encoded structural subunits of human OXPHOS complexes. As an example, all the known human nuclear structural complex I cDNA sequences have rapidly appeared in the literature. In more recent years, with the almost complete human genome draft in the authors' hands, a variety of mol. genetic approaches were used to unravel the nuclear gene defects in OXPHOS disorders. In this chapter the authors will review the tremendous progress in this area. The authors will briefly consider nuclear mitochondrial disorders in

OXPHOS related proteins. The authors will also present recent knowledge in 2 disorders assocd. with a defective nuclear-mitochondrial cross-talk. Their mol. basis is becoming clear to the mitochondrial science community. Finally, the authors will introduce the OXPHOS as a key player in the process of neurodegeneration in an increasing no. of disorders not originally classified as mitochondrial but later proved to be assocd. with an abnormal OXPHOS function.
RE.CNT 111 THERE ARE 111 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 5 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:327505 CAPLUS <<LOGINID::20080906>>
DN 141:167343
TI Imatinib induces mitochondria-dependent apoptosis of the Bcr-Abl positive K562 cell line and its differentiation towards the erythroid lineage. [Erratum to document cited in CA140:070546]
AU Jacquel, Arnaud; Herrant, Magali; Legros, Laurence; Belhacene, Nathalie; Luciano, Frederic; Pages, Gilles; Hofman, Paul; Auberger, Patrick
CS INSERM U526, Physiopathologie de la Survie et de la Mort Cellulaires et Infections Virales, Fac. de Medecine, Equipe Labellisee par la Ligue Nationale contre le Cancer, Nice, 06107, Fr.
SO FASEB Journal (2003), 17(15), 2347 CODEN: FAJOEC; ISSN: 0892-6638
PB Federation of American Societies for Experimental Biology
DT Journal
LA English
AB The cor. doi is: 10.1096/fj.03-0322.

L26 ANSWER 6 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2004:29456 CAPLUS <<LOGINID::20080906>>
DN 140:281960
TI Mitochondrial protein synthesis defects result in coordinate changes in gene expression as assessed by cDNA microarray
AU Kerstann, Keith William
CS Emory Univ., Atlanta, GA, USA
SO (2003) 168 pp. Avail.: UMI, Order No. DA3080333 From: Diss. Abstr. Int., B 2003, 64(2), 526
DT Dissertation
LA English
AB Unavailable

L26 ANSWER 7 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:940653 CAPLUS <<LOGINID::20080906>>
DN 140:299891
TI Gene-specific chromatin damage in human spermatozoa can be blocked by antioxidants that target mitochondria
AU Lamond, Scott; Watkinson, Michael; Rutherford, Tim; Laing, Ken; Whiting, Andrew; Smallwood, Alan; Nargund, Geeta; Campbell, Stuart; Banerjee, Subhasis
CS Department of Obstetrics and Gynaecology, St. George's Hospital Medical School, London, SW17 0RE, UK
SO Reproductive BioMedicine Online (2003), 7(4), 407-418 CODEN: RBOEA6; ISSN: 1472-6483
PB Reproductive Healthcare Ltd.
DT Journal
LA English
AB Incubation of gradient purified human spermatozoa, which are routinely maintained in media prior to IVF and intracytoplasmic sperm injection (ICSI), induced DNA strand breaks (up to 89 nicks .times. 10-3 bp) and chromatin release. Unlike highly dispersed Alu repeat sequences, the centromeric heterochromatin was much less susceptible to endonuclease attack. In addn. to chromatin release, the permeability of the sperm membrane was altered as evidenced by reduced accessibility of sperm nuclei to decondensation factors in mouse embryo exts. Hybridization of cDNA microarrays with DNA released from spermatozoa revealed a consistent hypersensitivity of certain genes to endogenous cleavage including TP53, VHL (tumor suppressors), BRCA1 (breast cancer), NOS1 (neurotransmitter), PECAM1, FLT1 (angiogenesis) and CDKN1C (cell cycle/imprinted). N-tent-Bu hydroxylamine (NTBH), a deriv. of the anti-teratogenic .alpha.-phenyl-N-t-Bu nitrone (PBN) and synthetic superoxide dismutase (SOD)/catalase mimetics inhibited chromatin release and sustained or dissipated relative mitochondrial membrane potential. Together, these results show a link between the hyperactivation of sperm mitochondria and chromosomal damage of specific genes in vitro, and that the potential risk of disruption of paternally contributed genes can be circumvented by antioxidants which are known to target mitochondria.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 8 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:926162 CAPLUS <<LOGINID::20080906>>
DN 140:88507
TI Response of genes associated with mitochondrial function to mild heat stress in yeast Saccharomyces cerevisiae
AU Sakaki, Kenjiro; Tashiro, Kosuke; Kuhara, Satoru; Mihara, Katsuyoshi
CS Department of Molecular Biology, Graduate School of Medical Science, Kyushu University, Japan
SO Journal of Biochemistry (Tokyo, Japan) (2003), 134(3), 373-384 CODEN: JOBIAO; ISSN: 0021-924X
PB Japanese Biochemical Society
DT Journal
LA English
AB The genome-wide expression pattern of budding yeast Saccharomyces. cerevisiae in response to mild heat treatment in a non-fermentable carbon source was analyzed using DNA microarrays. Of 5,870 open reading frames (nuclear genome transcripts) examd., 104 genes were upregulated and 287 genes were downregulated upon shifting of the cells from 25.degree.C to 37.degree.C. Forty upregulated genes and 235 downregulated genes encoded localization-assigned proteins. Of 113 heat-repressible genes (excluding 122 heat-repressible ribosomal genes), 36 were mitochondria-related genes, whereas only 2 of 40 heat-inducible genes were mitochondria-related. In particular, 9 genes involved in the mitochondrial respiratory chain and 7 genes involved in mitochondrial protein translocation were significantly repressed, suggesting that mitochondrial respiratory function and biogenesis were downregulated. Consistent with these findings, the growth of yeast cells in a non-fermentable carbon source was repressed at 37.degree.C and the mitochondria isolated from heat-stressed cells exhibited compromised preprotein-import activity compared with those from unstressed cells. In contrast, many genes involved in glycolysis and the metabolic pathway to produce glutamate via the tricarboxylic acid cycle, which is essential for biosynthetic reactions, were upregulated. Yeast cells might down-regulate mitochondrial function to circumvent heat-induced oxidative stress, upregulate stress-related genes, and remodel genes for metabolic pathways in response to mild heat stress: an adaptive response at the expense of cell growth.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 9 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:897248 CAPLUS <<LOGINID::20080906>>
DN 140:70546
TI Imatinib induces mitochondria-dependent apoptosis of the Bcr-Abl positive K562 cell line and its differentiation towards the erythroid lineage
AU Jacquel, Arnaud; Herrant, Magali; Legros, Laurence; Belhacene, Nathalie; Luciano, Frederic; Pages, Gilles; Hofman, Paul; Auberger, Patrick
CS INSERM U526, Physiopathologie de la Survie et de la Mort Cellulaires et Infections Virales, Equipe Labellisee par la Ligue Nationale contre le Cancer, Fac. de Medecine, Nice, 06107, Fr.
SO FASEB Journal (2003), 17(14), 2160-2162, 10.1096/fj.03-0322fje CODEN: FAJOEC; ISSN: 0892-6638
PB Federation of American Societies for Experimental Biology
DT Journal
LA English
AB Imatinib has emerged as the lead compd. for clin. development against chronic myeloid leukemia. Imatinib inhibits the kinase activity of Bcr-Abl, which functions by enhancing the proliferation of hematopoietic precursors and protecting them against apoptosis. Imatinib induces apoptosis of Bcr-Abl pos. cells, but how the drug effectively kills these cells remains partially understood. We show here that in K562 cells imatinib (i) abolished Bcr-Abl phosphorylation and activity and as a consequence Erk1/2, JNK, and AKT activation; (ii) induced mitochondrial transmembrane permeability dissipation; (iii) activated caspases 3, 9, and 8, demonstrating that the effect of imatinib is integrated at the mitochondrial level; and (iv) triggered caspase-dependent cleavage of Bcr-Abl. Interestingly, imatinib-mediated apoptosis was accompanied by erythroid differentiation of K562 cells. Moreover, phorbol esters inhibited imatinib-induced cell death and promoted differentiation toward the megakaryocytic lineage. Finally, we detd. by c-DNA array anal. that more than 20 genes were modulated by imatinib. These genes are involved in both cell death and differentiation programs, and some of them have never been reported before to be expressed or involved in erythroid differentiation. Our results demonstrate that imatinib is responsible for a major modification of the genetic program resulting in death and/or differentiation of K562 cells.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 10 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:891541 CAPLUS <<LOGINID::20080906>>
DN 140:196337
TI Microarray analysis of E2Fa-DPa-overexpressing plants uncovers a cross-talking genetic network between DNA replication and nitrogen assimilation
AU Vlieghe, Kobe; Vuylsteke, Marnik; Florquin, Kobe; Rombauts, Stephane; Maes, Sara; Ormenese, Sandra; Van Hummelen, Paul; Van de Peer, Yves; Inze, Dirk; De Veylder, Lieven
CS Department of Plant Systems Biology, Flanders Interuniversity Institute for Biotechnology (VIB), Ghent University, Ghent, B-9052, Belg.
SO Journal of Cell Science (2003), 116(20), 4249-4259 CODEN: JNCSAI; ISSN: 0021-9533
PB Company of Biologists Ltd.
DT Journal
LA English
AB Previously we have shown that overexpression of the heterodimeric E2Fa-DPa transcription factor in Arabidopsis thaliana results in ectopic cell division, increased endoreduplication, and an early arrest in development. To gain a better insight into the phenotypic behavior of E2Fa-DPa transgenic plants and to identify E2Fa-DPa target genes, a transcriptomic microarray anal. was performed. Out of 4,390 unique genes, a total of 188 had a twofold or more up- (84) or down-regulated (104) expression level in E2Fa-DPa transgenic plants compared to wild-type lines. Detailed promoter anal. allowed the identification of novel E2Fa-DPa target genes, mainly involved in DNA replication. Secondarily induced genes encoded proteins involved in cell wall biosynthesis, transcription and signal transduction or had an unknown function. A large no. of metabolic genes were modified as well, among which, surprisingly, many genes were involved in nitrate assimilation. Our data suggest that the growth arrest obsd. upon E2Fa-DPa overexpression results at least partly from a nitrogen drain to the nucleotide synthesis pathway, causing decreased synthesis of other nitrogen compds., such as amino acids and storage proteins.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 11 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:828931 CAPLUS <<LOGINID::20080906>>
DN 140:37241
TI Expression changes in mRNAs and mitochondrial damage in lens epithelial cells with selenite
AU Belusko, P. B.; Nakajima, T.; Azuma, M.; Shearer, T. R.
CS Senju Laboratory of Ocular Sciences, Senju Pharmaceutical Co. Ltd., Beaverton, OR, USA
SO Biochimica et Biophysica Acta, General Subjects (2003), 1623(2-3), 135-142 CODEN: BBGSB3; ISSN: 0304-4165
PB Elsevier B.V.
DT Journal
LA English
AB An overdose of sodium selenite induces cataracts in young rats. The mid-stage events producing the cataract include calpain-induced hydrolysis and pptn. of lens proteins. Apoptosis in lens epithelial cells has been suggested as an initial event in selenite cataracts. Expression levels of two genes assocd. with apoptosis were altered in lens epithelial cells from selenite-injected rats. The purpose of the present expt. was to perform a more comprehensive search for changes in expression of mRNAs in lens epithelial cells in order to more fully delineate the early events in selenite-induced cataracts. Lens epithelial cells were harvested at 1 and 2 days after a single s.c. injection of sodium selenite (30 .mu.mol/kg body wt.) into 12-day-old rats. Gene expression was analyzed using a com. DNA array (Rat Genome U34A GeneChip array, Affymetrix). Of approx. 8000 genes assayed by hybridization, 13 genes were decreased and 27 genes were increased in the rat lens epithelial cells after injection of selenite. Some of the up-regulated genes included apoptosis-related genes, and a majority of the down-regulated genes were mitochondrial genes. Previously obsd. changes in expression of EGR-1 mRNA were also confirmed. Changes in the expression patterns of mRNAs were also confirmed by RT-PCR. To det. the mechanism for damage of lens epithelial cells (alpha TN4 cell) by culture in selenite, leakage of cytochrome c from mitochondria was measured. Selenite caused significant leakage of cytochrome c into the cytosol of alpha TN4 cells. Our data suggested that the loss of integrity of lens epithelial cells by selenite might be caused by preferential down-regulation of mitochondrial RNAs, release of cytochrome c, and impaired mitochondrial function. Up-regulation of mRNAs involved in

maintenance of DNA, regulation of metab., and induction of apoptosis may also play roles.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 12 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:783894 CAPLUS <<LOGINID::20080906>>
DN 139:393913
TI Potentiation of cellular antioxidant capacity by Bcl-2: implications for its antiapoptotic function
AU Jang, Jung-Hee; Surh, Young-Joon
CS College of Pharmacy, Laboratory of Biochemistry and Molecular Toxicology, Seoul National University, Seoul, 151-742, S. Korea
SO Biochemical Pharmacology (2003), 66(8), 1371-1379 CODEN: BCPCA6; ISSN: 0006-2952
PB Elsevier Science B.V.
DT Journal; General Review
LA English
AB A review. A substantial body of data from clin. and lab. studies indicates that reactive oxygen intermediates are implicated in the pathogenesis of diverse human diseases, including cancer, diabetes, and neurodegenerative disorders. Oxidative stress induced by reactive oxygen intermediates often causes cell death via apoptosis that is regulated by a plenty of functional genes and their protein products. Bcl-2, which is an integral inter- ***mitochondrial*** membrane protein, blocks apoptosis induced by a wide ***array*** of death signals. In spite of extensive research, the mol. milieu that characterizes the antiapoptotic function of Bcl-2 is complex and not fully identified. Recently, there are several lines of evidence that Bcl-2 functions via antioxidant pathways to prevent apoptosis. Thus, bcl-2-overexpressing cells exhibit elevated expression of antioxidant enzymes and higher levels of cellular GSH compared with the control cells transfected with the vector alone. There has been increasing evidence supporting that the redox-sensitive transcription factor nuclear factor .kappa.B regulates the activity and/or expression of antioxidative and antiapoptotic target genes and promotes cell survival against oxidative cell death. This commentary focuses on the antioxidative functions of Bcl-2 and underlying mol. mechanisms in relation to its antiapoptotic property. The role of Bcl-2 in regulation of nuclear factor .kappa.B signaling pathways and possible cross-talk with mitogen-activated protein kinases are also discussed.
RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 13 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:778548 CAPLUS <<LOGINID::20080906>>
DN 139:376807
TI The role of the 3' untranslated region in mRNA sorting to the vicinity of mitochondria is conserved from yeast to human cells
AU Sylvestre, J.; Margeot, A.; Jacq, C.; Dujardin, G.; Corral-Debrinski, M.
CS Laboratoire de Genetique Moleculaire, Unite Mixte Recherche Centre National de la Recherche Scientifique 8541, Ecole Normale Superieure, Paris, Fr.
SO Molecular Biology of the Cell (2003), 14(9), 3848-3856 CODEN: MBCEEV; ISSN: 1059-1524
PB American Society for Cell Biology
DT Journal
LA English
AB We recently demonstrated, using yeast DNA ***microarrays*** , that mRNAs of polysomes that coisolate with ***mitochondria*** code for a subset of mitochondrial proteins. The majority of these mRNAs encode proteins of prokaryotic origin. Herein, we show that a similar assocn. occurs between polysomes and mitochondria in human cells. To det. whether mRNA transport machinery is conserved from yeast to human cells, we examd. the subcellular localization of human OXA1 mRNA in yeast. Oxa1p is a key component in the biogenesis of mitochondrial inner membrane and is conserved from bacteria to eukaryotic organelles. The expression of human OXA1 cDNA partially restores the respiratory capacity of yeast oxa1- cells. In this study, we demonstrate that 1) OXA1 mRNAs are remarkably enriched in mitochondrion-bound polysomes purified from yeast and human cells; 2) the presence of the human OXA1 3' untranslated region (UTR) is required for the function of the human Oxa1p inside yeast mitochondria; and 3) the accurate sorting of the human OXA1 mRNA to the vicinity of yeast mitochondria is due to the recognition of the human 3' UTR of OXA1 mRNA by yeast proteins. Therefore, it seems that the recognition mechanism of OXA1 3' UTR is conserved throughout evolution and is necessary for Oxa1p function.
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 14 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:756714 CAPLUS <<LOGINID::20080906>>
DN 139:243966
TI Mitochondrial proteome: Altered cytochrome c oxidase subunit levels in prostate cancer
AU Herrmann, Paul C.; Gillespie, John W.; Charboneau, Lu; Bichsel, Verena E.; Paweletz, Cloud P.; Calvert, Valerie S.; Kohn, Elise C.; Emmert-Buck, Michael R.; Liotta, Lance A.; Petricoin, Emanuel F., III
CS FDA-NCI Clinical Proteomics Program, Laboratory of Pathology, NIH, Bethesda, MD, USA
SO Proteomics (2003), 3(9), 1801-1810 CODEN: PROTC7; ISSN: 1615-9853
PB Wiley-VCH Verlag GmbH & Co. KGaA
DT Journal
LA English
AB Laser capture microdissection was combined with reverse phase protein lysate ***arrays*** to quant. analyze the ratios of ***mitochondrial*** encoded cytochrome c oxidase subunits to nuclear encoded cytochrome c oxidase subunits, and to correlate the ratios with malignant progression in human prostate tissue specimens. Cytochrome c oxidase subunits I-III comprise the catalytic core of the enzyme and are all synthesized from mitochondrial DNA. The remaining subunits (IV-VIII) are synthesized from cellular nuclear DNA. A significant ($P < 0.001$, 30/30 prostate cases) shift in the relative concns. of nuclear encoded cytochrome c oxidase subunits IV, Vb, and VIc compared to mitochondrial encoded cytochrome c oxidase subunits I and II was noted during the progression of prostate cancer from normal epithelium through premalignant lesions to invasive carcinoma. Significantly, this shift was discovered to begin even in the premalignant stage. Reverse phase protein lysate array-based observations were corroborate with immunohistochem., and extended to a few human carcinomas in addn. to prostate. This anal. points to a role for nuclear DNA encoded mitochondrial proteins in carcinogenesis; underscoring their potential as targets for therapy while highlighting the need for full characterization of the mitochondrial proteome.

RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 15 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:749675 CAPLUS <<LOGINID::20080906>>
DN 139:259378
TI NF-E2-related Factor-2 Mediates Neuroprotection against Mitochondrial Complex I Inhibitors and Increased Concentrations of Intracellular Calcium in Primary Cortical Neurons
AU Lee, Jong-Min; Shih, Andy Y.; Murphy, Timothy H.; Johnson, Jeffrey A.
CS Sch. Pharm., Univ. Wisconsin, Madison, WI, 53705-2222, USA
SO Journal of Biological Chemistry (2003), 278(39), 37948-37956 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB NF-E2-related factor-2 (Nrf2) regulates the gene expression of phase II detoxification enzymes and antioxidant proteins through an enhancer sequence referred to as the antioxidant-responsive element (ARE). In this study, the authors demonstrate that Nrf2 protects neurons in mixed primary neuronal cultures contg. both astrocytes (.apprx.10%) and neurons (.apprx.90%) through coordinate up-regulation of ARE-driven genes. Nrf2-/- neurons in this mixed culture system were more sensitive to mitochondrial toxin (1-methyl-4-phenyl-1,2,5,6-tetrahydropyridine or rotenone)-induced apoptosis compared with Nrf2+/+ neurons. To understand the underlying mechanism of this obsd. differential sensitivity, the authors compared the gene expression profiles using oligonucleotide microarrays. Microarray data showed that Nrf2+/+neuronal cultures had higher expression levels of genes encoding detoxification enzymes, antioxidant proteins, calcium homeostasis proteins, growth factors, neuron-specific proteins, and signaling mols. compared with Nrf2-/- neuronal cultures. As predicted from the microarray data, Nrf2-/- neurons were indeed more vulnerable to the cytotoxic effects of ionomycin- and 2,5-di-(t-butyl)-1,4-hydroquinone-induced increases in intracellular calcium. Finally, adenoviral vector-mediated overexpression of Nrf2 recovered ARE-driven gene expression in Nrf2-/- neuronal cultures and rescued Nrf2-/- neurons from rotenone- or ionomycin-induced cell death. Taken together, these findings suggest that Nrf2 plays an important role in protecting neurons from toxic insult.
RE.CNT 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 16 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:749662 CAPLUS <<LOGINID::20080906>>
DN 139:346687
TI The SIN3 Deacetylase Complex Represses Genes Encoding Mitochondrial Proteins: implications for the regulation of energy metabolism
AU Pile, Lori A.; Spellman, Paul T.; Katzenberger, Rebeccah J.; Wassarman, David A.
CS NICHD, Cell Biol. Metab. Branch, Natl. Inst. Health, Bethesda, MD, 20892, USA
SO Journal of Biological Chemistry (2003), 278(39), 37840-37848 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Deacetylation of histones by the SIN3 complex is a major mechanism utilized in eukaryotic organisms to repress transcription. Presumably, developmental and cellular phenotypes resulting from mutations in SIN3 are a consequence of altered transcription of SIN3 target genes. Therefore, to understand the mol. mechanisms underlying SIN3 mutant phenotypes in Drosophila, the authors used full-genome oligonucleotide microarrays to compare gene expression levels in wild type Drosophila tissue culture cells vs. SIN3-deficient cells generated by RNA interference. Of the 13,137 genes tested, 364 were induced and 35 were repressed by loss of SIN3. The .apprx.10-fold difference between the no. of induced and repressed genes suggests that SIN3 plays a direct role in regulating these genes. The identified genes are distributed throughout euchromatic regions but are preferentially excluded from heterochromatic regions of Drosophila chromosomes suggesting that the SIN3 complex can only access particular chromatin structures. A no. of cell cycle regulators were repressed by loss of SIN3, and functional studies indicate that repression of string, encoding the Drosophila homolog of the yeast CDC25 phosphatase, contributes to the G2 cell cycle delay of SIN3-deficient cells. Unexpectedly, a substantial fraction of genes induced by loss of SIN3 is involved in cytosolic and mitochondrial energy-generating pathways and other genes encode components of the mitochondrial translation machinery. Increased expression of mitochondrial proteins in SIN3-deficient cells is manifested in an increase in mitochondrial mass. Thus, SIN3 may play an important role in regulating mitochondrial respiratory activity.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 17 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:641689 CAPLUS <<LOGINID::20080906>>
DN 140:70843
TI Biochemical and microarray analyses of bupivacaine-induced apoptosis
AU Unami, Akira; Shinohara, Yasuo; Ichikawa, Tomokazu; Baba, Yoshinobu
CS Faculty of Pharmaceutical Sciences, The University of Tokushima, Tokushima, 770-8505, Japan
SO Journal of Toxicological Sciences (2003), 28(2), 77-94 CODEN: JTSCDR; ISSN: 0388-1350
PB Japanese Society of Toxicology
DT Journal
LA English
AB The mechanism by which apoptosis is induced by local anesthetic bupivacaine, a potent uncoupler of mitochondrial oxidative phosphorylation, was investigated. In promyelocytic leukemia cells HL-60, bupivacaine induced formation of apoptotic bodies and DNA fragmentation in a time- and dose-dependent manner similar to typical apoptosis inducers. Caspase-3, -8 and -9, which play a pivotal role in the initiation and execution of receptor- or mitochondria-mediated apoptosis, were all clearly activated by bupivacaine in good correlation with the degree of DNA fragmentation. However, bupivacaine did not induce either mitochondria permeability transition (PT) or release of cytochrome c in expts. with isolated mitochondria. These results suggest that an indirect action of bupivacaine on mitochondria occurs and that other mechanisms may be involved in bupivacaine-induced apoptosis. To obtain addnl. information concerning the mechanism of action involved in bupivacaine-induced apoptosis, a microarray anal. of gene expression in bupivacaine-treated HL-60 cells was carried out. Several

apoptosis-related genes were found to be transcriptionally regulated by bupivacaine using a high-d. cDNA microarray. The expression levels of heat shock protein 70 (HSP70), c-jun and c-fos genes were remarkably up-regulated and those of c-myc and poly (ADP ribose) polymerase (PARP) were down-regulated in bupivacaine-treated cells. These results are of value in developing a better understanding of the mol. mechanism of bupivacaine-induced apoptosis leading to neuro- or myotoxicity.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 18 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:624822 CAPLUS <<LOGINID::20080906>>
DN 139:287152
TI Long mRNAs coding for yeast mitochondrial proteins of prokaryotic origin preferentially localize to the vicinity of mitochondria
AU Sylvestre, Julien; Vialette, Stephane; Debrinski, Marisol Corral; Jacq, Claude
CS Laboratoire de Genetique Moleculaire, Ecole Normale Superieure, Paris, 75230, Fr.
SO GenomeBiology (2003), 4(7), No pp. given CODEN: GNBLFW; ISSN: 1465-6914 URL: http://genomebiology.com/content/pdf/gb-2003-4-7-r44.pdf
PB BioMed Central Ltd.
DT Journal; (online computer file)
LA English
AB Subcellular mRNA localization is important in most eukaryotic cells, even in unicellular organisms like yeast for which this process has been underestimated. Microarrays are rarely used to study subcellular mRNA localization at whole-genome level, but can be adapted to that purpose. This work focuses on studying the repartition of yeast nuclear transcripts encoding mitochondrial proteins between free cytosolic polysomes and polysomes bound to the mitochondrial outer membrane. Combining biochem. fractionations with oligonucleotide array analyses permits clustering of genes on the basis of the subcellular sites of their mRNA translation. A large fraction of yeast nuclear transcripts known to encode mitochondrial proteins is found in mitochondrial outer-membrane-bound fractions. These results confirm and extend a previous anal. conducted with partial genomic microarrays. Interesting statistical relations among mRNA localization, gene origin and mRNA lengths were found: longer and older mRNAs are more prone to be localized to the vicinity of mitochondria. These observations are included in a refined model of mitochondrial protein import. Mitochondrial biogenesis requires concerted expression of the many genes whose products make up the organelle. In the absence of any clear transcriptional program, coordinated mRNA localization could be an important element of the time-course of organelle construction. We have built a 'MitoChip' localization database from our results which allows us to identify interesting genes whose mRNA localization might be essential for mitochondrial biogenesis in most eukaryotic cells. Moreover, many components of the exptl. and data-anal. strategy implemented here are of general relevance in global transcription studies.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 19 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:623486 CAPLUS <<LOGINID::20080906>>
DN 139:336079
TI Increased expression of genes encoding mitochondrial proteins in papillary thyroid carcinomas
AU Faksvag Haugen, Dagny R.; Fluge, Oystein; Reigstad, Laila J.; Varhaug, Jan Erik; Lillehaug, Johan R.
CS Department of Oncology, Haukeland University Hospital, Bergen, Norway
SO Thyroid (2003), 13(7), 613-620 CODEN: THYRER; ISSN: 1050-7256
PB Mary Ann Liebert, Inc.
DT Journal
LA English
AB To investigate differences in gene expression between normal thyroid tissue and papillary thyroid carcinomas, the authors performed differential display (DD) polymerase chain reaction (PCR) using total RNA from fresh-frozen surgically removed thyroid specimens. Four DD fragments that were overexpressed in tumor tissue were identified as parts of genes from the mitochondrial genome: NAD (NADH) dehydrogenase 5, ATP synthase 6, cytochrome b, and cytochrome c oxidase I. The expression profiles of these genes were confirmed by hybridization using a DNA dot-blot array and radioactively labeled complex cDNA probes generated from tumor (30 biopsies) and nontumor (15 biopsies) total RNA. Cytochrome c oxidase III was also found to be overexpressed in papillary carcinomas, while the nuclear-encoded mitochondrial transcription factor A showed similar mRNA expression levels in tumor and nontumor tissue. Electron microscopy showed increased no. and size of mitochondria in papillary carcinomas. Immunohistochem. using a monoclonal antibody recognizing a nuclear-encoded mitochondrial protein showed positivity in all cases of papillary carcinoma (44 samples), while normal thyroid tissue (34 samples) was neg. in all cases except 3, in which there was a weak, focal cytoplasmic staining. The authors conclude that papillary thyroid carcinomas show increased expression of mitochondrial mRNA and proteins, encoded by nuclear as well as mitochondrial genes.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 20 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:613939 CAPLUS <<LOGINID::20080906>>
DN 139:243428
TI PGC-1.beta. in the regulation of hepatic glucose and energy metabolism
AU Lin, Jiandie; Tarr, Paul T.; Yang, Ruojing; Rhee, James; Puigserver, Pere; Newgard, Christopher B.; Spiegelman, Bruce M.
CS Dana-Farber Cancer Institute and the Department of Cell Biology, Harvard Medical School, Boston, MA, 02115, USA
SO Journal of Biological Chemistry (2003), 278(33), 30843-30848 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Peroxisome proliferator-activated receptor .gamma. coactivator-1.alpha. (PGC-1.alpha.) is a transcriptional coactivator that regulates multiple aspects of cellular energy metab., including mitochondrial biogenesis, hepatic gluconeogenesis, and .beta.-oxidn. of fatty acids. PGC-1.alpha. mRNA levels are increased in both type-1 and type-2 diabetes and may contribute to elevated hepatic glucose prodn. in diabetic states. We have recently described PGC-1.beta., a novel transcriptional coactivator that is a homolog of PGC-1.alpha.. Although PGC-1.beta. shares significant sequence similarity and tissue distribution with PGC-1.alpha., the biol. activities of PGC-1.beta. in the regulation of cellular metab. is unknown. In this study, we used an adenoviral-

mediated expression system to study the function of PGC-1.beta. both in cultured hepatocytes and in the liver of rats. PGC-1.beta., like PGC-1.alpha., potently induces the expression of an ***array*** of ***mitochondrial*** genes involved in oxidative metab. However, in contrast to PGC-1.alpha., PGC-1.beta. poorly activates the expression of gluconeogenic genes in hepatocytes or liver in vivo, illustrating that these two coactivators play distinct roles in hepatic glucose metab. The reduced ability of PGC-1.beta. to induce gluconeogenic genes is due, at least in part, to its inability to phys. assoc. with and coactivate hepatic nuclear receptor 4.alpha. (HNF4.alpha.) and forkhead transcription factor O1 (FOXO1), two crit. transcription factors that mediate the activation of gluconeogenic gene expression by PGC-1.alpha.. These data illustrate that PGC-1.beta. and PGC-1.alpha. have distinct arrays of activities in hepatic energy metab.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 21 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:571325 CAPLUS <<LOGINID::20080906>>
DN 139:96360
TI Protein and cDNA sequences of 20.24-kilodalton human mitochondrial aspartate aminotransferase-like protein and their therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1363673 A 20020814 CN 2001-105091 20010105
PRAI CN 2001-105091 20010105
AB The invention provides protein and cDNA sequences of a novel 20.24-kilodalton human protein, designated as "mitochondrial aspartate aminotransferase 20.24", which has similar expression pattern to that of known mitochondrial aspartate aminotransferase. The invention relates to expression of mitochondrial aspartate aminotransferase-like protein in E. coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against mitochondrial aspartate aminotransferase-like protein. The invention further relates to the uses of the mitochondrial aspartate aminotransferase-like protein in treatment of mitochondrial aspartate aminotransferase-related diseases.

L26 ANSWER 22 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:519320 CAPLUS <<LOGINID::20080906>>
DN 139:177892
TI Profiling gene transcription reveals a deficiency of mitochondrial oxidative phosphorylation in Trypanosoma cruzi-infected murine hearts: implications in chagasic myocarditis development
AU Garg, Nisha; Popov, Vsevolod L.; Papaconstantinou, John
CS Department of Microbiology and Immunology, University of Texas Medical Branch, Galveston, TX, 77555, USA
SO Biochimica et Biophysica Acta, Molecular Basis of Disease (2003), 1638(2), 106-120 CODEN: BBADEX; ISSN: 0925-4439
PB Elsevier B.V.
DT Journal
LA English
AB In this study, we report the host genetic responses that characterize Trypanosoma cruzi-induced myocarditis in a murine model of infection and disease development. The mRNA species from the myocardium of infected mice were assessed using cDNA microarray technol. at immediate early, acute, and chronic stages of infection. The immediate early reaction of the host to T. cruzi infection was marked by up-regulation of transcripts indicative of proinflammatory and interferon-induced immune responses. Following acute infection, overexpression of transcripts for extracellular matrix (ECM) proteins, possibly initiated in response to myocardial injuries by invading and replicating parasites, was suggestive of active reparative and remodeling reactions. Surprisingly, progression to the cardiac disease phase was assocd. with coordinated down-regulation of a majority (>70%) of the differentially expressed genes. Among the most repressed genes were the troponins, essential for contractile function of the myofibrils, and the genes encoding components of oxidative phosphorylation (OXPHOS) pathways. Reverse transcription-polymerase chain reaction (RT-PCR), Western blotting, and biochem. assays confirmed the microarray results and provided evidence for the deficiency of OXPHOS complex IV in the chagasic murine heart. We discuss the apparent role of OXPHOS dysfunction in the cardiac hypertrophic and remodeling processes with the development of chagasic cardiomyopathy (CCM).
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 23 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:500896 CAPLUS <<LOGINID::20080906>>
DN 140:317786
TI A Small Molecule Suppressor of FK506 that Targets the Mitochondria and Modulates Ionic Balance in Saccharomyces cerevisiae
AU Butcher, Rebecca A.; Schreiber, Stuart L.
CS Department of Chemistry and Chemical Biology, Howard Hughes Medical Institute, Harvard University, Cambridge, MA, 02138, USA
SO Chemistry & Biology (2003), 10(6), 521-531 CODEN: CBOLE2; ISSN: 1074-5521
PB Cell Press
DT Journal
LA English
AB FK506 inhibits the evolutionarily conserved, Ca2+-dependent phosphatase calcineurin, which in yeast is essential for growth during sodium stress. We undertook a chem. genetic modifier screen to identify small mols. that suppress the ability of FK506 to inhibit yeast growth in high NaCl. One of these small mol. suppressors, SFK1 (suppressor of FK506 1), causes a mitochondrially induced death in low salt, concomitant with the release of reactive oxygen species. Biochem., SFK1 interacts with Por1p, a channel protein in the outer mitochondrial membrane, suggesting that SFK1 interacts with the mitochondria directly. A genome-wide screen of yeast deletion strains for hypersensitivity to SFK1 yielded several strains with impaired mitochondrial function, as well as several with reduced sodium tolerance. Our data link ionic balance to mitochondrial function and suggest a role for calcineurin in mediating this signaling network.
RE.CNT 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 24 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:465621 CAPLUS <<LOGINID::20080906>>
DN 139:256587
TI Transcription profiling reveals mitochondrial, ubiquitin and signaling systems abnormalities in postmortem brains from subjects with a history of alcohol abuse or dependence
AU Sokolov, Boris P.; Jiang, Lixin; Trivedi, Niraj S.; Aston, Christopher
CS Molecular Neuropsychiatry Branch, National Institute on Drug Abuse, National Institutes of Health, Baltimore, MD, USA
SO Journal of Neuroscience Research (2003), 72(6), 756-767
CODEN: JNREDK; ISSN: 0360-4012
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Alc. abuse is a common human disorder with high rate of comorbidity with other psychiatric disorders. To identify candidate mechanisms for alc. abuse, the expression of 12,626 genes was measured in postmortem temporal cortex from 11 subjects with a history of alc. abuse or dependence, with or without other psychiatric diagnoses and compared pairwise with the expression in 11 nonalcoholic subjects matched for the other psychiatric diagnoses and demographics. Genes were defined to have altered expression in alc. abuse if: (1) the gene showed decreased expression in at least 10 of 11 subjects with alc. abuse, or showed increased expression in at least 10 of 11 subjects with this diagnosis compared to matched non-abusers ($P < 0.007$, .chi.2test); or (2) the difference in the mean abuser/non-abuser ratio for the gene from value of 1.0 was significant at $P < 0.05$ (one sample t-test). In subjects with a history of alc. abuse or dependence, 163 genes were changed significantly. The most abundant and consistent changes were in gene families encoding mitochondrial proteins, the ubiquitin system, and signal transduction. These alterations indicate disturbances in energy metab. and multiple signaling mechanisms in the temporal cortex of subjects with a history of alc. abuse or dependence. We hypothesize that these mechanisms may be related to alc. abuse traits or long-term effects of alc.
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 25 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:450969 CAPLUS <<LOGINID::20080906>>
DN 139:2073
TI Protein and cDNA sequences of a 11-kilodalton human mitochondrial translational initiation factor-like protein and their therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1361122 A 20020731 CN 2000-136304 20001226
PRAI CN 2000-136304 20001226
AB The invention provides protein and cDNA sequences of a novel 11-kilodalton human protein, designated as "mitochondrial translational initiation factor 11", which has similar expression pattern to that of known mitochondrial translational initiation factor. The invention relates to expression of mitochondrial translational initiation factor-like protein in E. coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against mitochondrial translational initiation factor-like protein. The invention further relates to the uses of the mitochondrial translational initiation factor-like protein in treatment of mitochondrial translational initiation factor-related diseases (such as neoplasm, blood disease, HIV infection, immune disease, and inflammation).

L26 ANSWER 26 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:427943 CAPLUS <<LOGINID::20080906>>
DN 139:208334
TI Design of oligonucleotide arrays to detect point mutations: molecular typing of antibiotic resistant strains of Neisseria gonorrhoeae and hantavirus infected deer mice
AU Booth, Stephanie A.; Drebot, Michael A.; Martin, Irene E.; Ng, Lai-King
CS Population and Public Health Branch, National Microbiology Laboratory, Health Canada, Winnipeg, MB, Can.
SO Molecular and Cellular Probes (2003), 17(2-3), 77-84
CODEN: MCPRE6; ISSN: 0890-8508
PB Elsevier Science Ltd.
DT Journal
LA English
AB Microarrays are promising tools for use in mol. diagnostics due to their ability to perform a multitude of tests simultaneously. In the case of genotyping many such tests will require discrimination of sequence at the single nucleotide level. A no. of challenges exist including binding of optimal quantities of probe to the chip surface, the use of uniform hybridization conditions across the chip and the generation of labeled target. The authors investigated two model systems to test out the efficacy and ease with which probes can be designed for this purpose. In the first of these the authors designed primers to identify five mutations found in two genes from N. gonohorroeae, gyrA and parC that have been implicated in ciprofloxacin resistance. In the second system the authors used a similar strategy to identify four mutations in AT rich mitochondrial DNA from deer mice. These mutations are assocd. with deer mice subspecies that originate from different geog. regions of Canada and harbor different hantavirus strains. In every case the authors were able to design probes that could discriminate mutations in the target sequences under uniform hybridization conditions, even when targets were fairly long in length, up to 400 bp. The results suggest that microarray anal. of point mutations might be very useful for automated identification and characterization of pathogens and their hosts.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 27 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:423879 CAPLUS <<LOGINID::20080906>>
DN 139:318065
TI Detection of heteroplasmy in human head hair and bloodstains using a ***mitochondrial*** DNA linear ***array*** assay
AU Roberts, Katherine Anne
CS City Univ. of New York, New York, NY, USA
SO (2002) 202 pp. Avail.: UMI, Order No. DA3063874 From: Diss. Abstr. Int., B 2003, 63(9), 4035

DT Dissertation
LA English
AB Unavailable

L26 ANSWER 28 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:405325 CAPLUS <<LOGINID::20080906>>
DN 139:161747
TI Towards an analysis of the rice mitochondrial proteome
AU Heazlewood, Joshua L.; Howell, Katharine A.; Whelan, James; Millar, A. Harvey
CS Plant Molecular Biology Group, School of Biomedical and Chemical Sciences, The University of Western Australia, Crawley, 6009, Australia
SO Plant Physiology (2003), 132(1), 230-242 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Purified rice (Oryza sativa) ***mitochondrial*** proteins have been ***arrayed*** by isoelec. focusing/PAGE (PAGE), by blue-native (BN) PAGE, and by reverse-phase high-performance liq. chromatog. (LC) sepn. (LC-mass spectrometry [MS]). From these protein ***arrays*** , we have identified a range of rice ***mitochondrial*** proteins, including hydrophilic/hydrophobic proteins (grand av. of hydropathicity = -1.27 to +0.84), highly basic and acid proteins (isoelec. point = 4.0-12.5), and proteins over a large mol. mass range (6.7-252 kDa), using proteomic approaches. BN PAGE provided a detailed picture of electron transport chain protein complexes. A total of 232 protein spots from isoelec. focusing/PAGE and BN PAGE sepns. were excised, trypsin digested, and analyzed by tandem MS (MS/MS). Using this dataset, 149 of the protein spots (the products of 91 nonredundant genes) were identified by searching translated rice open reading frames from genomic sequence and six-frame translated rice expressed sequence tags. Sequence comparison allowed us to assign functions to a subset of 85 proteins, including many of the major function categories expected for this organelle. A further six spots were matched to rice sequences for which no specific function has yet been detd. Complete digestion of mitochondrial proteins with trypsin yielded a peptide mixt. that was analyzed directly by reverse-phase LC via org. solvent elution from a C-18 column (LC-MS). These data yielded 170 MS/MS spectra that matched 72 sequence entries from open reading frame and expressed sequence tag databases. Forty-five of these were obtained using LC-MS alone, whereas 28 proteins were identified by both LC-MS and gel-based sepns. In total, 136 nonredundant rice proteins were identified, including a new set of 23 proteins of unknown function located in plant mitochondria. We also report the first direct identification, to our knowledge, of PPR (pentatricopeptide repeat) proteins in the plant mitochondrial proteome. This dataset provides the first extensive picture, to our knowledge, of mitochondrial functions in a model monocot plant.
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 29 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:377312 CAPLUS <<LOGINID::20080906>>
DN 139:83426
TI Human ***mitochondrial*** complex I deficiency: Investigating transcriptional responses by ***microarray***
AU van der Westhuizen, F. H.; van den Heuvel, L. P.; Smeets, R.; Veltman, J. A.; Pfundt, R.; van Kessel, A. G.; Ursing, B. M.; Smeitink, J. A. M.
CS Nijmegen Center for Mitochondrial Disorders, Department of Pediatrics, University Medical Center, Nijmegen, Neth.
SO Neuropediatrics (Stuttgart, Germany) (2003), 34(1), 14-22 CODEN: NRPDDB; ISSN: 0174-304X
PB Georg Thieme Verlag
DT Journal
LA English
AB NADH:ubiquinone oxidoreductase (complex I) deficiency is one of the most frequently encountered defects of the mitochondrial energy generating system. A deficiency of this enzyme complex leads to a wide variety in clin. disease expression. The cell biol. consequences of such mutations, however, are poorly understood. We investigated transcriptional responses in fibroblast cell lines harboring mutations in the 5 different nuclear DNA encoded subunits using a ***mitochondria*** -targeting ***microarray*** . Expression profiles of cell lines cultured under conditions that favor glycolytic metab. were compared to profiles when cultured under conditions favoring oxidative metab. Approx. 60 genes displayed differential expression under these conditions in either all mutated cell lines or selected cell lines only. A marked induction of metallothioneins as well as ATP1G1 transcripts was detected in all patient cell lines. Transcriptional responses such as the induction of heat shock protein transcripts, decreased PDK1, BNIP3 and mitochondrial genome encoding gene transcripts occurred in selected patient cell lines. The obsd. transcript profile points to a common, putative defensive, response relating to oxidative stress. Although further investigations of other human OXPHOS system diseases is warranted, these results clearly underline that functional genomics holds for the study of inherited metabolic disease.
RE.CNT 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 30 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:334512 CAPLUS <<LOGINID::20080906>>
DN 138:350783
TI Enzyme-amplified redox microarray detection process and microarray device
IN Dill, Killian
PA USA
SO U.S. Pat. Appl. Publ., 26 pp., Cont.-in-part of U.S. Ser. No. 944,727. CODEN: USXXCO
DT Patent
LA English
FAN.CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 20030082601 A1 20030501 US 2002-229755 20020827
PRAI US 2001-944727 A2 20010830
AB There is disclosed a process and an array for assaying for binding of target mols. to capture mols. on microarray devices, wherein the microarray devices contain electrodes. Specifically, there is disclosed a binding (including nucleotide hybridization) process to detect binding on a microarray wherein the microarray contains electronically addressable electrode devices. There is further disclosed an enzymically catalyzed oxidn./redn. reaction to take place within a "virtual flask" region of a microarray wherein the reaction is detected by current changes detected on the addressable electrode. Antibodies were immobilized on

microarray devices and the corresponding analytes were detected using secondary antibodies conjugated with horseradish peroxidase.

L26 ANSWER 31 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:229732 CAPLUS <<LOGINID::20080906>>
DN 139:115234
TI Reovirus-induced apoptosis: a minireview
AU Clarke, P.; Tyler, K. L.
CS Department of Neurology, Denver, CO, 80220, USA
SO Apoptosis (2003), 8(2), 141-150 CODEN: APOPFN; ISSN: 1360-8185
PB Kluwer Academic Publishers
DT Journal; General Review
LA English
AB A review. Reoviruses infect a variety of mammalian hosts and serve as an important exptl. system for studying the mechanisms of virus-induced injury. Reovirus infection induces apoptosis in cultured cells in vitro and in target tissues in vivo, including the heart and central nervous system (CNS). In epithelial cells, reovirus-induced apoptosis involves the release of tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) from infected cells and the activation of TRAIL-assocd. death receptors (DRs) DR4 and DR5. DR activation is followed by activation of caspase 8, cleavage of Bid, and the subsequent release of pro-apoptotic mitochondrial factors. By contrast, in neurons, reovirus-induced apoptosis involves a wider ***array*** of DRs, including TNFR and Fas, and the ***mitochondria*** appear to play a less crit. role. These results show that reoviruses induce apoptotic pathways in a cell and tissue specific manner. In vivo there is an excellent correlation between the location of viral infection, the presence of tissue injury and apoptosis, indicating that apoptosis is a crit. mechanism by which disease is triggered in the host. These studies suggest that inhibition of apoptosis may provide a novel strategy for limiting virus-induced tissue damage following infection.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 32 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:223338 CAPLUS <<LOGINID::20080906>>
DN 138:363761
TI Transcript profiling of human platelets using microarray and serial analysis of gene expression
AU Gnatenko, Dmitri V.; Dunn, John J.; McCorkle, Sean R.; Weissmann, David; Perrotta, Peter L.; Bahou, Wadie F.
CS Department of Medicine, State University of New York, Stony Brook, NY, 11794-8151, USA
SO Blood (2003), 101(6), 2285-2293 CODEN: BLOOAW; ISSN: 0006-4971
PB American Society of Hematology
DT Journal
LA English
AB Human platelets are anucleate blood cells that retain cytoplasmic mRNA and maintain functionally intact protein translational capabilities. We have adapted complementary techniques of microarray and serial anal. of gene expression (SAGE) for genetic profiling of highly purified human blood platelets. Microarray anal. using the Affymetrix HGU95Av2 approx. 12 600-probe set maximally identified the expression of 2147 (range, 13%-17%) platelet-expressed transcripts, with approx. 22% collectively involved in metab. and receptor/signaling, and an over representation of genes with unassigned function (32%). In contrast, a modified SAGE protocol using the Type IIS restriction enzyme MmeI (generating 21-base pair [bp] or 22-bp tags) demonstrated that 89% of tags represented mitochondrial (mt) transcripts (enriched in 16S and 12S rRNAs), presumably related to persistent mt-transcription in the absence of nuclear-derived transcripts. The frequency of non-mt SAGE tags paralleled av. difference values (relative expression) for the most "abundant" transcripts as detd. by microarray anal., establishing the concordance of both techniques for platelet profiling. Quant. reverse transcription-polymerase chain reaction (PCR) confirmed the highest frequency of mt-derived transcripts, along with the mRNAs for neurogranin (NGN, a protein kinase C substrate) and the complement lysis inhibitor clusterin among the top 5 most abundant transcripts. For confirmatory characterization, immunoblots and flow cytometric analyses were performed, establishing abundant cell-surface expression of clusterin and intracellular expression of NGN. These observations demonstrate a strong correlation between high transcript abundance and protein expression, and they establish the validity of transcript anal. as a tool for identifying novel platelet proteins that may regulate normal and pathol. platelet (and/or megakaryocyte) functions.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 33 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:222412 CAPLUS <<LOGINID::20080906>>
DN 138:216540
TI Human 35.97-kDa mitochondrial translation initiation factor IF-2 like protein and its cDNA and therapeutic use
IN Mao, Yumin; Xie, Yi
PA Shanghai Biowindow Gene Development Inc., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1351056 A 20020529 CN 2000-125819 20001026
PRAI CN 2000-125819 20001026
AB The invention provides protein and cDNA sequences for a novel human 35.97-kDa protein cloned from human fetal brain, which shares a similar mRNA expression pattern to mitochondrial translation initiation factor IF-2, thus called IF-2mt35.97. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The invention further relates to applications of related gene or protein products for the treatment of related diseases, such as myocardial infarction, metabolic cataract, infection, diabetes mellitus, neoplasm, and etc. Methods of screening for related analogs, agonists, inhibitors, and antagonists and using them as therapeutic drugs are also described.

L26 ANSWER 34 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:218843 CAPLUS <<LOGINID::20080906>>
DN 139:1152
TI Dehydroepiandrosterone affects the expression of multiple genes in rat liver including 11.beta.-hydroxysteroid dehydrogenase type 1: A cDNA array analysis

AU Gu, Shi; Ripp, Sharon L.; Prough, Russell A.; Geoghegan, Thomas E.
CS Department of Biochemistry and Molecular Biology, The University of Louisville School of Medicine, Louisville, KY, USA
SO Molecular Pharmacology (2003), 63(3), 722-731 CODEN: MOPMA3; ISSN: 0026-895X
PB American Society for Pharmacology and Experimental Therapeutics
DT Journal
LA English
AB Dehydroepiandrosterone (DHEA) is a C-19 adrenal steroid precursor to the gonadal steroids. In humans, circulating levels of DHEA, as its sulfated conjugate, are high at puberty and throughout early adulthood but decline with age. Dietary supplementation to maintain high levels of DHEA purportedly has beneficial effects on cognitive memory, the immune system, and fat and carbohydrate metab. In rodents, DHEA is a peroxisome proliferator that induces genes for the classical peroxisomal and microsomal enzymes assocd. with this response. These effects are mediated through activation of peroxisome proliferator-activated receptor .alpha. (PPAR.alpha.). However, DHEA can affect the expression of genes independently of PPAR.alpha., including the gene for the major inducible drug and xenobiotic metabolizing enzyme, cytochrome P 450 3A23. To elucidate the biochem. assocd. with DHEA treatment, we employed a cDNA gene expression array using liver RNA from rats treated with DHEA or the classic peroxisome proliferator nafenopin. Principal components anal. identified 30 to 35 genes whose expression was affected by DHEA and/or nafenopin. Some were genes previously identified as PPAR-responsive genes. Changes in expression of several affected genes were verified by quant. reverse transcriptase-polymerase chain reaction. These included aquaporin 3, which was induced by DHEA and to a lesser extent nafenopin, nuclear tyrosine phosphatase, which was induced by both agents, and 11.beta.-hydroxysteroid dehydrogenase 1, which was decreased by treatment with DHEA in a dose-dependent fashion. Regulation of 11.beta.- hydroxysteroid dehydrogenase 1 expression is important since the enzyme is believed to amplify local glucocorticoid signaling, and its repression may cause some of the metabolic effects assocd. with DHEA.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 35 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:206469 CAPLUS <<LOGINID::20080906>>
DN 139:18092
TI Phylogenetic and genomic analysis of the complete mitochondrial DNA sequence of the spotted asparagus beetle Crioceris duodecimpunctata
AU Stewart, James Bruce; Beckenbach, Andrew T.
CS Department of Molecular Biology and Biochemistry, Simon Fraser University, Burnaby, BC, V5A 1S6, Can.
SO Molecular Phylogenetics and Evolution (2003), 26(3), 513-526 CODEN: MPEVEK; ISSN: 1055-7903
PB Elsevier Science
DT Journal
LA English
AB We report the complete mitochondrial DNA sequence of the spotted asparagus beetle, Crioceris duodecimpunctata. The genome complement, gene order, and nucleotide compn. of this beetle's mitochondrial genome were found to be typical of those reported for other insects. Unusual features of this genome include the substitution of UCU for GCU as the anticodon for tRNASer, an unusual T.psi.C loop for the tRNAIle gene, and the identification of a putative ATT start codon for cox1. The utility of complete mitochondrial genome data for phylogenetic inference of the insect orders was tested, and compared to that of cox1 and combined mitochondrial ribosomal DNA sequences. Even though the no. of insect orders represented by complete mitochondrial genomes is still limited, several well-established relationships are evident in the phylogenetic anal. of the complete sequences. Monophyly of the orders Diptera, Lepidoptera, and Coleoptera were consistently recovered. Monophyly of the Holometabola was also obsd. in some (though not all) analyses. The accumulation of complete ***mitochondrial*** sequences from a broader ***array*** of insect orders holds the promise of clarifying the early diversification of insects.
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 36 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:176884 CAPLUS <<LOGINID::20080906>>
DN 138:367082
TI Genome-wide cDNA microarray analysis of gene-expression profiles involved in ovarian endometriosis
AU Arimoto, Takahide; Katagiri, Toyomasa; Oda, Katsutoshi; Tsunoda, Tatsuhiko; Yasugi, Toshiharu; Osuga, Yutaka; Yoshikawa, Hiroyuki; Nishii, Osamu; Yano, Tetsu; Taketani, Yuji; Nakamura, Yusuke
CS Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, The University of Tokyo, Minato-ku, Tokyo, 108-8639, Japan
SO International Journal of Oncology (2003), 22(3), 551-560 CODEN: IJONES; ISSN: 1019-6439
PB International Journal of Oncology
DT Journal
LA English
AB Using a cDNA microarray consisting of 23,040 genes, the authors analyzed gene-expression profiles of ovarian endometrial cysts from 23 patients to identify genes involved in endometriosis. By comparing expression patterns between endometriotic tissues and corresponding eutopic endometria, the authors identified 15 genes that were commonly upregulated in the endometrial cysts during both proliferative and secretory phases of the menstrual cycle, 42 that were upregulated only in the proliferative phase, and 40 that were up-regulated only in the secretory phase. The up-regulated elements included genes encoding some HLA antigens, complement factors, ribosomal proteins, and TGFBI. 337 Genes were commonly down-regulated throughout the menstrual cycle, 144 only in the proliferative phase, and 835 only in the secretory phase. The down-regulated elements included the tumor suppressor TP53, genes related to apoptosis such as GADD34, GADD45A, GADD45B and PIG11, and the gene encoding OVGP1, a protein involved in maintenance of early pregnancy. Semi-quant. RT-PCR expts. supported the results of the authors' microarray anal. These data should provide useful information for finding candidate genes whose products might serve as mol. targets for diagnosis or treatment of endometriosis.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 37 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:155954 CAPLUS <<LOGINID::20080906>>

DN 138:182089
TI Human 29.7-kDa mitochondrial DNA polymerase like protein and its cDNA and therapeutic use
IN Mao, Yumin; Xie, Yi
PA Shanghai Biowindow Gene Development, Inc., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 32 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1345939 A 20020424 CN 2000-125549 20000929
PRAI CN 2000-125549 20000929
AB The invention provides protein and cDNA sequences for a novel human 29.7-kDa protein cloned from human fetal brain, which shares a similar mRNA expression pattern to mitochondrial DNA polymerase. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The invention further relates to applications of related gene or protein products for the treatment of related diseases, such as myocardial infarction, metabolic cataract, infection, diabetes mellitus, and neoplasm. Methods of screening for related analogs, agonists, inhibitors, and antagonists and using them as therapeutic drugs are also described.

L26 ANSWER 38 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:137991 CAPLUS <<LOGINID::20080906>>
DN 138:398700
TI Genomic and proteomic analysis of mitochondrial carrier proteins in Arabidopsis
AU Millar, A. Harvey; Heazlewood, Joshua L.
CS Plant Molecular Biology Group, School of Biomedical and Chemical Sciences, The University of Western Australia, Crawley, 6009, Australia
SO Plant Physiology (2003), 131(2), 443-453 CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Biologists
DT Journal
LA English
AB Plant mitochondria maintain metabolic communication with the cytosol through a family of carrier proteins. In Arabidopsis, a subset of 45 putative genes encoding members of this family have been identified based on generalized mitochondrial carrier features. No gene clusters are apparent and few of the predicted protein products have mitochondrial targeting sequences recognized by bioinformatic predictors. Only nine genes are currently represented by more than 10 expressed sequence tags at The Institute for Genomic Research. Analyses of public microarray expts. reveal differential expression profiles of the more highly expressed members of this gene family in different plant organs and in response to plant hormone application and environmental stresses. A comparison of this Arabidopsis carrier subset (45) to the yeast gene family (35) reveals 10 orthologous groups between the two species. Recent surveys of the Arabidopsis mitochondrial proteome by two-dimensional gel sepns. have not identified any of these carrier proteins, presumably because of their hydrophobicity and basicity. Isolating integral membrane proteins from Arabidopsis mitochondria, using one-dimensional electrophoresis for protein sepn. and tandem mass spectrometry-based sequencing of doubly charged peptides, we have unequivocally identified specific carrier gene products located in mitochondria. This approach has identified six of the nine carriers represented highly in expressed sequence tag databases: adenine nucleotide translocator (At3g8580 and At5g13490), dicarboxylate/tricarboxylate carrier (At5g19760), phosphate carrier (At5g14040), uncoupling protein (At3g54110), and a carrier gene of unknown function (At4g01100). Overall, the combined transcript and protein expression data indicates that only a small subset of the carrier family of genes provide the majority of carrier proteins of Arabidopsis mitochondria.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 39 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:134829 CAPLUS <<LOGINID::20080906>>
DN 138:315343
TI Polymorphism ratio sequencing: A new approach for single nucleotide polymorphism discovery and genotyping
AU Blazej, Robert G.; Paegel, Brian M.; Mathies, Richard A.
CS San Francisco Joint Bioengineering Graduate Group, University of California, Berkeley, CA, 94720, USA
SO Genome Research (2003), 13(2), 287-293 CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Polymorphism ratio sequencing (PRS) combines the advantages of high-throughput DNA sequencing with new labeling and pooling schemes to produce a powerful assay for sensitive single nucleotide polymorphism (SNP) discovery, rapid genotyping, and accurate, multiplexed allele frequency detn. In the PRS method, dideoxy-terminator extension ladders generated from a sample and ref. template are labeled with different energy-transfer fluorescent dyes and coinjected into a sepn. capillary for comparison of relative signal intensities. The authors demonstrate the PRS method by screening two human ***mitochondrial*** genomes for sequence variations using a microfabricated capillary ***array*** electrophoresis device. A titrn. of multiplexed DNA samples places the limit of minor allele frequency detection at 5%. PRS is a sensitive and robust polymorphism detection method for the anal. of individual or multiplexed samples that is compatible with any four-color fluorescence DNA sequencer.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 40 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:79546 CAPLUS <<LOGINID::20080906>>
DN 138:331994
TI Mitochondrial biogenesis and remodeling during adipogenesis and in response to the insulin sensitizer rosiglitazone
AU Wilson-Fritch, Leanne; Burkart, Alison; Bell, Gregory; Mendelson, Karen; Leszyk, John; Nicoloro, Sarah; Czech, Michael; Corvera, Silvia
CS Program in Molecular Medicine, Interdisciplinary Graduate Program, University of Massachusetts Medical School, Worcester, MA, 01615, USA
SO Molecular and Cellular Biology (2003), 23(3), 1085-1094 CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English

AB White adipose tissue is an important endocrine organ involved in the control of whole-body metab., insulin sensitivity, and food intake. To better understand these functions, 3T3-L1 cell differentiation was studied by using combined proteomic and genomic strategies. The proteomics approach developed here exploits velocity gradient centrifugation as an alternative to isoelec. focusing for protein sepn. in the first dimension. A 20- to 30-fold increase in the concn. of numerous mitochondrial proteins was obsd. during adipogenesis, as detd. by mass spectrometry and database correlation anal. Light and electron microscopy confirmed a large increase in the no. of mitochondrion profiles with differentiation. Furthermore, mRNA profiles obtained by using Affymetrix GeneChips revealed statistically significant increases in the expression of many nucleus-encoded mitochondrial genes during adipogenesis. Qual. changes in mitochondrial compn. also occur during adipose differentiation, as exemplified by increases in expression of proteins involved in fatty acid metab. and of mitochondrial chaperones. Furthermore, the insulin sensitizer rosiglitazone caused striking changes in mitochondrial shape and expression of selective mitochondrial proteins. Thus, although mitochondrial biogenesis has classically been assocd. with brown adipocyte differentiation and thermogenesis, our results reveal that mitochondrial biogenesis and remodeling are inherent to adipose differentiation per se and are influenced by the actions of insulin sensitizers.
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 41 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2003:8197 CAPLUS <<LOGINID::20080906>>
DN 138:50845
TI Protein and cDNA sequences of human mitochondrial cytochrome bc1 complex core protein II 12.21 and therapeutical uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1340524 A 20020320 CN 2000-119831 20000831
PRAI CN 2000-119831 20000831
AB The invention provides the protein and cDNA sequences of a novel human mitochondrial cytochrome bc1 complex core protein II 12.21 with the mol. wt. of 12 kilodaltons cloned from human fetal brain. In particular, the invention discloses that the gene encoding this protein has a similar gene expression pattern with gene encoding mitochondrial cytochrome bc1 complex core protein II. The invention also relates to construction of mitochondrial cytochrome bc1 complex core protein II 12.21 expression vector for prepn. of recombinant protein using prokaryotes or eukaryotes. The invention relates to prepn. of antibody against this protein. The invention further relates to the PCR primers, nucleic acid probes, DNA fragments and protein agonists or antagonists specific for this gene or gene product for the diagnosis as well as treatment of various diseases, such as neoplasm, blood disease, development disorder, HIV infection, immune disease, inflammation, etc.

L26 ANSWER 42 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:944384 CAPLUS <<LOGINID::20080906>>
DN 138:232657
TI Phylogenetic analyses of the Lyophylleae (Agaricales, Basidiomycota) based on nuclear and mitochondrial rDNA sequences
AU Hofstetter, Valerie; Clemencon, Heinz; Vilgalys, Rytas; Moncalvo, Jean-Marc
CS Department of Ecology, University of Lausanne, Switz.
SO Mycological Research (2002), 106(9), 1043-1059 CODEN: MYCRER; ISSN: 0953-7562
PB Cambridge University Press
DT Journal
LA English
AB Current classifications of the Lyophylleae and the importance of siderophilous granulation in the basidia for the classification of agaricoid fungi were evaluated using parsimony analyses of sequence data from the nuclear ribosomal large subunit gene (nLSU), the internal transcribed spacer region of the nuclear ribosomal ***array*** (ITS), and the ***mitochondrial*** ribosomal small subunit gene (mtSSU). These three different data partitions were phylogenetically congruent on the basis of the Mickevich-Farris statistical test, but not from the ILD and the Templeton tests. Bootstrap supports for nodes in phylogenetic trees generated from combined nLSU, ITS, and mtSSU sequence data were generally higher than those in trees generated from individual data sets. This suggests a lack of major conflict in the phylogenetic signal among the different data sets. We conclude that the Mickevich-Farris test is more appropriate for estg. congruence and combinability between different sources of mol. data than the more widely used ILD and Templeton tests, at least when the different data sets have their resp. resoln. power at different depths in the phylogeny. Results of the combined analyses show that the Entolomataceae are a sister group to a clade composed of the Lyophylleae, Termitomyceteae, and Tricholomateae p.p. This implies that presence of siderophilous granulation in the basidia of agaric fungi has probably a single origin, and would have been lost in the Tricholomateae. Inclusion of the Termitomyceteae within the Lyophylleae suggests homol. of the macro type granulation. Because the exact placement of Tricholomateae pro parte remains uncertain, it remains unclear whether the Lyophylleae (including Termitomyceteae) are monophyletic or paraphyletic. Within the Lyophylleae, genera Lyophyllum and Calocybe are shown to be artificial, as are Lyophyllum sections Lyophyllum, Difformia, and Tephrophana. Four main natural groups of Lyophylleae have been identified that should serve as a basis for developing a more natural classification system for these fungi.
RE.CNT 85 THERE ARE 85 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 43 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:942991 CAPLUS <<LOGINID::20080906>>
DN 138:50843
TI Protein and cDNA sequences of human mitochondrial translation initiation factor 20.90 and therapeutical uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 35 pp. CODEN: CNXXEV
DT Patent
LA Chinese

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- -------
PI CN 1340522 A 20020320 CN 2000-119823 20000831
PRAI CN 2000-119823 20000831
AB The invention provides the protein and cDNA sequences of a novel human mitochondrial translation initiation factor 20.90 with the mol. wt. of 21 kilodaltons cloned from human fetal brain. In particular, the invention discloses that the gene encoding this protein has a similar gene expression pattern with gene encoding mitochondrial translation initiation factor. The invention also relates to construction of mitochondrial translation initiation factor 20.90 expression vector for prepn. of recombinant protein using prokaryotes or eukaryotes. The invention relates to prepn. of antibody against this protein. The invention further relates to the PCR primers, nucleic acid probes, DNA fragments and protein agonists or antagonists specific for this gene or gene product for the diagnosis as well as treatment of various diseases, such as sugar-, lipid-, and protein-metab. disorder, etc.

L26 ANSWER 44 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:877822 CAPLUS <<LOGINID::20080906>>
DN 138:315610
TI Microarray profiling of skeletal muscle tissues from equally obese, non-diabetic insulin-sensitive and insulin-resistant Pima Indians
AU Yang, X.; Pratley, R. E.; Tokraks, S.; Bogardus, C.; Permana, P. A.
CS Clinical Diabetes and Nutrition Section, Phoenix Epidemiology and Clinical Research Branch, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Phoenix, AZ, 85016, USA
SO Diabetologia (2002), 45(11), 1584-1593 CODEN: DBTGAJ; ISSN: 0012-186X
PB Springer-Verlag
DT Journal
LA English
AB We carried out global transcript profiling to identify differentially expressed skeletal muscle genes in insulin resistance, a major risk factor for Type II (non-insulin-dependent) diabetes mellitus. This approach also complemented the ongoing genomic linkage analyses to identify genes linked to insulin resistance and diabetes in Pima Indians. We compared gene expression profiles of skeletal muscle tissues from 18 insulin-sensitive vs. 17 insulin-resistant equally obese, non-diabetic Pima Indians using oligonucleotide arrays consisting of about 40,600 transcripts of known genes and expressed sequence tags, and analyzed the results with the Wilcoxon rank sum test. We verified the mRNA expression of ten differentially (best-ranked) and ten similarly (worst-ranked) genes using quant. Real Time PCR. There were 185 differentially expressed transcripts by the rank sum test. The differential expressions of two out of the ten best-ranked genes were confirmed and the similar expressions of all ten worst-ranked genes were reproduced. Of the 185 differentially expressed transcripts, 20 per cent were true positives and some could generate new hypotheses about the etiol. or pathophysiol. of insulin resistance. Furthermore, differentially expressed genes in chromosomal regions with linkage to diabetes and insulin resistance serve as new diabetes susceptibility genes.
RE.CNT 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 45 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:870750 CAPLUS <<LOGINID::20080906>>
DN 138:134159
TI Specialization of midgut cells for synthesis of male isoprenoid pheromone components in two scolytid beetles, Dendroctonus jeffreyi and Ips pini
AU Nardi, J. B.; Young, A. Gilg; Ujhelyi, E.; Tittiger, C.; Lehane, M. J.; Blomquist, G. J.
CS Department of Entomology, University of Illinois, Urbana, IL, 61801, USA
SO Tissue & Cell (2002), 34(4), 221-231 CODEN: TICEBI; ISSN: 0040-8166
PB Elsevier Science Ltd.
DT Journal
LA English
AB Endodermal or midgut cells have only recently been recognized as the site of pheromone synthesis in bark beetles. Midgut cells are not only specialized for digestion, but they have also been recruited to form isoprenoid compds. that function as pheromone components in Ips pini and Dendroctonus jeffreyi. Male bark beetle midgut cells are competent to produce isoprenoid pheromones after feeding or stimulation by juvenile hormone (JH) III. Competent midgut cells share many ultrastructural features with cells that do not secrete isoprenoid pheromone, but they are distinguished from these by abundant and highly ordered arrays of smooth endoplasmic reticula. During secretion, both midgut cells that produce pheromone and cells that do not are characterized by the presence of apical extrusions (apocrine secretion) rather than the presence of vesicles that fuse with the apical membrane and undergo exocytosis (eccrine secretion). Pheromone-producing cells of the midgut do not represent a population of cells that are distinct from cells involved in digestion. All, or most, midgut cells of male I. pini and D. jeffreyi can secrete pheromones as well as digestive enzymes.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 46 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:815459 CAPLUS <<LOGINID::20080906>>
DN 138:149785
TI An immunocytochemical approach to detection of mitochondrial disorders
AU Hanson, Bonnie J.; Capaldi, Roderick A.; Marusich, Michael F.; Sherwood, Steven W.
CS Molecular Probes, Inc., Eugene, OR, USA
SO Journal of Histochemistry and Cytochemistry (2002), 50(10), 1281-1288 CODEN: JHCYAS; ISSN: 0022-1554
PB Histochemical Society, Inc.
DT Journal
LA English
AB ***Mitochondrial*** disorders can lead to a confusing ***array*** of symptoms, which frequently makes a diagnosis difficult. Traditional approaches to such diagnoses are based on enzyme activity assays, with further characterization provided by genetic anal. However, these methods require relatively large sample sizes, are time-consuming, labor-intensive, and show variability between labs. Here, we report an immunocytochem. test that makes use of monoclonal antibodies to subunits from each of the oxidative phosphorylation complexes and pyruvate dehydrogenase to aid in the detection of mitochondrial disorders. It can be completed and data analyzed in less than 4 h. We have used this test to study fibroblast cultures from patients with

mitochondrial disorders arising from both mitochondrial DNA and nuclear DNA defects. We have also examd. cases of Leigh syndrome arising from different genetic causes. We show that patients can be categorized on the basis of which complexes are affected and whether or not the defect being studied shows a mosaic distribution, an indicator of whether the causal mutation(s) is/are in the mitochondrial or nuclear genome. Immunocytochem. anal. as described here should be considered as an initial screen for mitochondrial disorders by which to direct (and limit) the subsequent enzymic and genetic tests required to make an unambiguous diagnosis.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 47 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:811809 CAPLUS <<LOGINID::20080906>>
DN 138:168003
TI State-dependent alterations in mitochondrial complex I activity in platelets: a potential peripheral marker for schizophrenia
AU Dror, N.; Klein, E.; Karry, R.; Sheinkman, A.; Kirsh, Z.; Mazor, M.; Tzukerman, M.; Ben-Shachar, D.
CS Department of Psychiatry, Laboratory of Psychobiology, Rambam Medical Center and B Rappaport Faculty of Medicine, Technion, Haifa, Israel
SO Molecular Psychiatry (2002), 7(9), 995-1001 CODEN: MOPSFQ; ISSN: 1359-4184
PB Nature Publishing Group
DT Journal
LA English
AB Schizophrenia, the most severe psychiatric disorder, is characterized by heterogeneity of clin. signs, often categorized into pos. and neg. symptoms. Among a wide ***array*** of competing biol. mechanisms, altered cerebral energy metab. and ***mitochondrial*** dysfunction have been suggested to play an important role in the pathophysiol. of schizophrenia. In this study we investigated mitochondrial complex I in platelets of 113 schizophrenic patients divided into three groups (acute psychotic episode, chronic active state and residual schizophrenia) and 37 control subjects. Complex I was analyzed at the level of enzymic activity, mRNA and protein levels by enzyme kinetics, RT-PCR and Western blot analyses, resp. Complex I activity in platelets of schizophrenic patients altered with disease state presenting high specificity and sensitivity. Thus, increased activity was assocd. with psychotic symptomol., while its decrease was obsd. in patients with residual schizophrenia. The relationship between the clin. state and complex I activity in schizophrenia was further supported by its pos. correlation with the severity of patients' pos. symptoms assessed by clin. ratings. In addn., similar alterations were obsd. at the levels of mRNA and protein of the 24- and 51-kDa iron-sulfur flavoprotein subunits of the complex. Taken together these results point to the potential of platelet complex I to turn into a reliable novel marker for schizophrenia. At present, definitive diagnosis depends only on descriptive behavioral and symptomatic information, therefore a peripheral measurable specific marker will contribute to diagnosis and monitoring of the disease.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 48 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:760441 CAPLUS <<LOGINID::20080906>>
DN 137:243097
TI Protein and cDNA sequences of a novel human mitochondrial creatine kinase subunit 22.11 and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 36 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1331091 A 20020116 CN 2000-116817 20000628
PRAI CN 2000-116817 20000628
AB The invention provides protein and cDNA sequences of a novel human protein, designated as "mitochondrial creatine kinase subunit 22.11", which has similar gene expression pattern with known human mitochondrial creatine kinase. The invention relates to expression of mitochondrial creatine kinase subunit 22.11 in E.coli BL21(DE3)plySs transfected with plasmid pET-28(+). The invention also relates to prepn. of antibody against mitochondrial creatine kinase subunit 22.11. The invention further relates to the uses of the mitochondrial creatine kinase subunit 22.11 fragment as probes in diagnosis, and in treatment of mitochondrial creatine kinase subunit 22.11-related diseases (such as sugar-, lipid-, and protein-metab. disorder).

L26 ANSWER 49 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:750007 CAPLUS <<LOGINID::20080906>>
DN 138:36783
TI Hepatobiliary pathology
AU Lefkowitch, Jay H.
CS College of Physicians and Surgeons of Columbia University, New York, NY, 10032, USA
SO Current Opinion in Gastroenterology (2002), 18(3), 290-298 CODEN: COGAEK; ISSN: 0267-1379
PB Lippincott Williams & Wilkins
DT Journal; General Review
LA English
AB A review. Technol. advances using cDNA ***microarray*** hybridization, liver diseases characterized by ***mitochondrial*** DNA depletion, and new work characterizing bile salt transport problems in familial intrahepatic cholestasis syndromes were some of the major highlights of this past year. Anal. of normal livers by cDNA microarrays disclosed 2418 unique gene transcripts encoding a host of cellular structural and functional proteins. This technique was also applied to hepatocellular carcinoma, where enhanced expression of a no. of genes involved in antiapoptosis and cell transformation may shed addnl. light on the process of hepatocarcinogenesis. Mitochondrial DNA depletion seen in Navajo neurohepatopathy and in respiratory chain disorders of infancy was assocd. with cholestasis and cirrhosis in the former and microvesicular steatosis and oncocytic transformation (mitochondrial hyperplasia) in the latter. Pathologists who routinely examine liver biopsies after liver or bone marrow transplantation should be aware of unusual biopsy features that mimic other diseases, such as the autoimmune hepatitis-like syndrome that may follow liver transplantation and chronic graft-vs.-host disease that clin. and pathol. resembles acute hepatitis.
RE.CNT 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 50 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:709683 CAPLUS <<LOGINID::20080906>>
DN 137:196657
TI Protein and cDNA sequences of human mitochondrial translation initiation factor 15.4 and therapeutical uses
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 34 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1326988 A 20011219 CN 2000-116381 20000607
WO 2002010213 A1 20020207 WO 2001-CN911 20010604
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2002010312 A 20020213 AU 2002-10312 20010604
PRAI CN 2000-116381 A 20000607 WO 2001-CN911 W 20010604
AB The invention provides the protein and cDNA sequences of a novel human mitochondrial translation initiation factor 15.4 with the mol. wt. of 15 kilodaltons cloned from human fetal brain. In particular, the invention discloses that the gene encoding this protein has a similar gene expression pattern with gene encoding mitochondrial translation initiation factor. The invention also relates to construction of mitochondrial translation initiation factor 15.4 expression vector for prepn. of recombinant protein using prokaryotes or eukaryotes. The invention relates to prepn. of antibody against this protein. The invention further relates to the PCR primers, nucleic acid probes, DNA fragments and protein agonists or antagonists specific for this gene or gene product for the diagnosis as well as treatment of metabolic disorders of carbohydrates, lipids and proteins.

L26 ANSWER 51 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:453381 CAPLUS <<LOGINID::20080906>>
DN 137:42629
TI Human mitochondria carrier protein 13 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Shanghai Bode Gene Development Co., Ltd., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1323810 A 20011128 CN 2000-115695 20000516
PRAI CN 2000-115695 20000516
AB The invention provides cDNA sequences of a novel human mitochondria carrier protein 13 called mCP13 cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 52 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:381763 CAPLUS <<LOGINID::20080906>>
DN 136:364942
TI Human mitochondrial carrier protein 18 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1315407 A 20011003 CN 2000-115210 20000328
WO 2001079508 A1 20011025 WO 2001-CN486 20010326
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2001063721 A 20011030 AU 2001-63721 20010326
PRAI CN 2000-115210 A 20000328 WO 2001-CN486 W 20010326
AB The invention provides cDNA sequences of a novel human mitochondrial carrier protein 18 (named by protein MW detected in SDS-PAGE gel, also called hmCP18) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 53 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:366470 CAPLUS <<LOGINID::20080906>>
DN 137:152883
TI Hypocrellins and hypericin induced apoptosis in human tumor cells: A possible role of hydrogen peroxide

AU Ali, Seyed Mohamed; Chee, Soo Khee; Yuen, Gan Yik; Olivo, Malini
CS Department of Medical Sciences, National Cancer Centre, School of Sciences, Singapore, Singapore
SO International Journal of Molecular Medicine (2002), 9(5), 461-472 CODEN: IJMMFG; ISSN: 1107-3756
PB International Journal of Molecular Medicine
DT Journal
LA English
AB We examd. whether generation of H2O2 is a crit. event for the apoptotic pathway upstream of mitochondrial involvement and caspase-3 protease activation. Perylquinone photosensitizers such as Hypocrellin A (HA), Hypocrellin B (HB) and Hypericin (HY) induced activation of caspase-3 and apoptosis upon photoactivation. Generation of H2O2 was commonly detected after photoactivation within an hour, and scavenging of H2O2 caused cells to fail to undergo apoptosis. Flow cytometry demonstrated that H2O2 prodn. preceded loss of mitochondrial membrane potential (.DELTA..psi.m) in photoactivated cells treated with HA, HB and HY. Then caspase-3 activity was activated, followed by DNA fragmentation. These findings suggest that HA, HB and HY upon photoactivation induce H2O2 generation, which causes (.DELTA..psi.m) and subsequently caspase-3 activation, resulting in apoptosis. These findings suggest that generation of H2O2 by photoactivation of HA, HB and HY causes activation of caspase-3. Therefore, H2O2 may function as a common mediator for apoptosis induced by HA, HB and HY. The present study also demonstrated that upon photoactivation HA, HB and HY induced a decrease in intracellular acidification, glutathione (GSH) depletion and an ***array*** of ***mitochondrial*** damage together with apoptotic morphol. changes in the irradiated cells.
RE.CNT 72 THERE ARE 72 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 54 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:350320 CAPLUS <<LOGINID::20080906>>
DN 137:320893
TI Microfabricated capillary array electrophoresis: high-throughput DNA sequencing and polymorphism analysis
AU Paegel, Brian M.; Emrich, Charles A.; Blazej, Robert G.; Elkin, Christopher J.; Scherer, James R.; Mathies, Richard A.
CS Department of Chemistry, University of California, Berkeley, CA, 94720, USA
SO Micro Total Analysis Systems 2001, Proceedings .mu.TAS 2001 Symposium, 5th, Monterey, CA, United States, Oct. 21-25, 2001 (2001), 462-464. Editor(s): Ramsey, J. Michael; Berg, Albert van den. Publisher: Kluwer Academic Publishers, Dordrecht, Neth. CODEN: 69COT6; ISBN: 1-4020-0148-7
DT Conference
LA English
AB Microfabricated capillary array electrophoresis (.mu.CAE) circuitry has been developed and optimized allowing high-throughput DNA sequencing and polymorphism anal. in a compact, circular, wafer-scale device. The 96-lane processor, which incorporates hyper-turns and fluidically balanced injectors, produces .apprx.41,000 bases of M13 extension products to an accuracy >99% (phred 20) in only 24 min. Polymorphism ratio sequencing (PRS) with the same device enables rapid scanning of the entire human mitochondrial genome in a single run.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 55 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:289134 CAPLUS <<LOGINID::20080906>>
DN 136:368331
TI Gene expression profiling in DQA1*0501+ children with untreated dermatomyositis: a novel model of pathogenesis
AU Tezak, Zivana; Hoffman, Eric P.; Lutz, Jennica L.; Fedczyna, Tamara O.; Stephan, Dietrich; Bremer, Eric G.; Krasnoselska-Riz, Irina; Kumar, Ajit; Pachman, Lauren M.
CS Research Center for Genetic Medicine, Children's National Medical Center, Washington, DC, USA
SO Journal of Immunology (2002), 168(8), 4154-4163 CODEN: JOIMA3; ISSN: 0022-1767
PB American Association of Immunologists
DT Journal
LA English
AB Juvenile dermatomyositis (JDM), the most common pediatric inflammatory myopathy, is a systemic vasculopathy affecting young children. Epidemiol. studies documenting an antecedent illness in the 3 mo before the first definite symptom (rash and/or weakness) of JDM are supported by immunol. data that suggest that the disease pathophysiol. is Ag driven. The purpose of this study was to compare the gene expression profiles in muscle biopsies of four untreated DQA1*0501+ JDM children with profiles from children with a known necrotizing myopathy (Duchenne muscular dystrophy), as well as an in vitro antiviral model (NF90), and healthy pediatric controls. Nearly half (47%) of the dysregulated genes in JDM were assocd. with the immune response. In particular, increased expression of IFN-.alpha..beta.-inducible genes 6-16, myxovirus resistance protein p78, latent cytosolic transcription factor, LMP2, and TAP1 was obsd. This profile is consistent with an IFN-.alpha..beta. transcription cascade seen in the in vitro viral resistance model. The IFN-.alpha..beta.-inducible profile was superimposed on transcription profiles reflective of myofiber necrosis and regeneration shared with Duchenne muscular dystrophy. Expressed genes were confirmed by quant. real-time PCR (6-16), immunofluorescence (thrombospondin 4), and immunolocalization (IFN-.gamma., p21). The authors hypothesize that these data support a model of Ag (viral) induction of an apparent autoimmune disease based on dynamic interaction between the muscle, vascular, and immune systems in the genetically susceptible (DQA1*0501+) child.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 56 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:286849 CAPLUS <<LOGINID::20080906>>
DN 136:289979
TI Human mitochondrial ATPase (coupling factor 6) sequence homolog hmATPaseCF6-10 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1314367 A 20010926 CN 2000-114976 20000317 WO 2001079424 A2 20011025 WO 2001-

CN330 20010316 WO 2001079424 A3 20020328 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 2001050243 A5 20011030 AU 2001-50243 20010316
PRAI CN 2000-114976 A 20000317 WO 2001-CN330 W 20010316
AB The invention provides cDNA sequences of a novel human mitochondrial ATPase (coupling factor 6) sequence homolog 10 (named by protein MW detected in SDS-PAGE gel, also called hmATPaseCF6-10) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 57 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:285102 CAPLUS <<LOGINID::20080906>>
DN 136:289970
TI Human mitochondrial transcription termination factor sequence homolog 42 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bode Gene Development Co., Ltd., Shanghai, Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 33 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI CN 1313294 A 20010919 CN 2000-111966 20000310
PRAI CN 2000-111966 20000310
AB The invention provides cDNA sequences of a novel human mitochondrial transcription termination factor sequence homolog 42 (named by protein MW detected in SDS-PAGE gel, also called mTERF42) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 58 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:234712 CAPLUS <<LOGINID::20080906>>
DN 136:398667
TI Plant mitochondria move on F-actin, but their positioning in the cortical cytoplasm depends on both F-actin and microtubules
AU Van Gestel, K.; Kohler, R. H.; Verbelen, J-P.
CS Department of Biology, University of Antwerp UIA, Wilrijk, 2610, Belg.
SO Journal of Experimental Botany (2002), 53(369), 659-667 CODEN: JEBOA6; ISSN: 0022-0957
PB Oxford University Press
DT Journal
LA English
AB Mitochondrion movement and positioning was studied in elongating cultured cells of tobacco (Nicotiana tabacum L.), contg. mitochondria-localized green fluorescent protein. In these cells, mitochondria are either actively moving in strands of cytoplasm transversing or bordering the vacuole, or immobile positioned in the cortical layer of cytoplasm. Depletion of the cell's ATP stock with the uncoupling agent DNP shows that the movement is much more energy demanding than the positioning. The active movement is F-actin based. It is inhibited by the actin filament disrupting drug latrunculin B, the myosin ATPase inhibitor 2,3-butanedione 2-monoxime and the sulphydryl-modifying agent N-ethylmaleimide. The microtubule disrupting drug oryzalin did not affect the movement of mitochondria itself, but it slightly stimulated the recruitment of cytoplasmic strands, along which mitochondria travel. The immobile mitochondria are often positioned along parallel lines, transverse or oblique to the cell axis, in the cortical cytoplasm of elongated cells. This positioning is mainly microtubule based. After complete disruption of the F-actin, the ***mitochondria*** parked themselves into conspicuous parallel ***arrays*** transverse or oblique to the cell axis or clustered around chloroplasts and around patches and strands of endoplasmic reticulum. Oryzalin inhibited all positioning of the ***mitochondria*** in parallel ***arrays*** .
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 59 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:220813 CAPLUS <<LOGINID::20080906>>
DN 136:258272
TI Genome arrays for hybridization analysis utilizing randomly selected nucleic acid fragments as probes
IN Shuster, Jeffrey; Hurban, Patrick; Woessner, Jeffrey
PA Paradigm Genetics, Inc., USA
SO PCT Int. Appl., 22 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2002022850 A2 20020321 WO 2001-US28782 20010912 WO 2002022850 A3 20030731 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR,

IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG AU 2001090938 A5 20020326 AU 2001-90938 20010912
PRAI US 2000-660663 A 20000913 US 2000-679760 A 20001005 WO 2001-US28782 W 20010912
AB Arrays comprised of elements of randomly selected nucleic acid fragments representing at least a portion of the genome from an organism or the genome of an organelle from an organism, together with methods for their prepn. and use, are described. The use of randomly selected fragments is to avoid either the labor needed to sequence large quantities of DNA or the bias towards strongly expressed genes introduced by the use of non-redundant sequences. Methods for calcn. of the no. of fragments of a given size needed to create a comprehensive probe arrays are described.

L26 ANSWER 60 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:215285 CAPLUS <<LOGINID::20080906>>
DN 136:290591
TI Applied proteomics. Mitochondrial proteins and effect on function
AU Lopez, Mary F.; Melov, Simon
CS Proteome Systems, Woburn, MA, 01801, USA
SO Circulation Research (2002), 90(4), 380-389 CODEN: CIRUAL; ISSN: 0009-7330
PB Lippincott Williams & Wilkins
DT Journal; General Review
LA English
AB A review with 129 refs. The identification of a majority of the polypeptides in mitochondria would be invaluable because they play crucial and diverse roles in many cellular processes and diseases. The endogenous prodn. of reactive oxygen species (ROS) is a major limiter of life as illustrated by studies in which the transgenic overexpression in invertebrates of catalytic antioxidant enzymes results in increased lifespans. Mitochondria have received considerable attention as a principal source and target of ROS. Mitochondrial oxidative stress has been implicated in heart disease including myocardial preconditioning, ischemia/reperfusion, and other pathologies. In addn., oxidative stress in the mitochondria is assocd. with the pathogenesis of Alzheimer's disease, Parkinson's disease, prion diseases, and amyotrophic lateral sclerosis (ALS) as well as aging itself. The rapidly emerging field of proteomics can provide powerful strategies for the characterization of mitochondrial proteins. Current approaches to mitochondrial proteomics include the creation of detailed catalogs of the protein components in a single sample or the identification of differentially expressed proteins in diseased or physiol. altered samples vs. a ref. control. It is clear that for any proteomics approach pre-fractionation of complex protein mixts. is essential to facilitate the identification of low-abundance proteins because the dynamic range of protein abundance within cells has been estd. to be as high as 107. The opportunities for identification of proteins directly involved in diseases assocd. with or caused by mitochondrial dysfunction are compelling. Future efforts will focus on linking genomic ***array*** information to actual protein levels in ***mitochondria*** .
RE.CNT 129 THERE ARE 129 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 61 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:205943 CAPLUS <<LOGINID::20080906>>
DN 136:337528
TI Genome-wide analysis of mRNAs targeted to yeast mitochondria
AU Marc, Philippe; Margeot, Antoine; Devaux, Frederic; Blugeon, Corinne; Corral-Debrinski, Marisol; Jacq, Claude
CS Laboratoire de Genetique Moleculaire (UMR CNRS 8541), Ecole Normale Superieure, Paris, F-75005, Fr.
SO EMBO Reports (2002), 3(2), 159-164 CODEN: ERMEAX; ISSN: 1469-221X
PB Oxford University Press
DT Journal
LA English
AB It is agreed that nuclear-encoded mitochondrial proteins are post-translationally targeted to mitochondria, even if, in some cases, a co-translational phase can assist the import of precursor proteins. The authors used yeast DNA ***microarrays*** to analyze the mRNA populations assocd. with free and ***mitochondrion*** -bound polysomes. As expected, many mRNAs, known to encode mitochondrial proteins, are localized to free cytoplasmic polysomes, but many are localized to mitochondrion-bound polysomes. Furthermore, the 3'-UTR of six randomly chosen mitochondrion-bound mRNAs contains sufficient information to target, in vivo, non-translatable RNA to the vicinity of mitochondria. Interestingly, genes producing mRNAs that are targeted to mitochondria are mainly of ancient bacterial origin, whereas those producing mRNAs that are translated in the cytoplasm are mainly of eukaryotic origin. These observations, which support the recent hypotheses concerning the dual origin of the mitochondrial proteome, provide new insights into the biogenesis of mitochondria.
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 62 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:168676 CAPLUS <<LOGINID::20080906>>
DN 137:163713
TI Caffeine Enhances the Calcium-Dependent Cardiac Mitochondrial Permeability Transition: Relevance for Caffeine Toxicity
AU Sardao, Vilma A.; Oliveira, Paulo J.; Moreno, Antonio J. M.
CS Centro de Neurociencias e Biologia Celular de Coimbra, Departamento de Zoologia, Faculdade de Ciencias e Technologia, Universidade de Coimbra, Coimbra, P-3004-517, Port.
SO Toxicology and Applied Pharmacology (2002), 179(1), 50-56 CODEN: TXAPA9; ISSN: 0041-008X
PB Academic Press
DT Journal
LA English
AB Caffeine (1,3,7-trimethylxanthine), a compd. present in beverages such as tea and coffee, is known to be toxic at high concns. Some of the obsd. clin. conditions include cardiovascular disease and reproductive disorders, among others. The possible toxic effects of caffeine on heart mitochondria are still poorly understood. The influence of caffeine on the mitochondrial permeability transition has not been clarified so far. The objective of this study was to investigate whether caffeine, at toxic concns., had any stimulating effect on the permeability transition of heart mitochondria isolated from Wistar rats, as well as whether it influenced mitochondrial respiratory parameters. Our results show that caffeine reduced mitochondrial ability to accumulate calcium by increasing the susceptibility of heart mitochondria to the opening of the transition pore. Caffeine not only hindered mitochondrial capacity to recover membrane potential after calcium addn. but also increased the rate of calcium-dependent mitochondrial swelling and calcium-induced

calcium release. The increased swelling was also obsd. in nonenergized mitochondria. Caffeine also showed a complex ***array*** of effects on heart ***mitochondrial*** bioenergetics, as evaluated by respiratory parameter measurements. We obsd. an increase in state 4 respiration and a depression in state 3 respiration, although no effect was obsd. on succinate-sustained mitochondrial membrane potential in the absence of calcium. Our work may be relevant to cardiovascular problems linked to caffeine toxicity and also to in vitro experiences involving caffeine-induced calcium release from the sarcoplasmic reticulum and uptake by mitochondria. (c) 2002 Academic Press.
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 63 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:159403 CAPLUS <<LOGINID::20080906>>
DN 136:178994
TI Protein and cDNA of novel human mitochondria-associated ribosomal protein L4 sequence homolog and uses in therapy
IN Mao, Yumin; Xie, Yi
PA Shanghai Shengyuan Gene Development Co., Ltd., Peop. Rep. China
SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 24 pp. CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1310185 A 20010829 CN 2000-111730 20000224
PRAI CN 2000-111730 20000224
AB The invention provides protein and cDNA sequences of one new human mitochondria-assocd. 60S ribosomal protein L4 sequence homolog cloned from human embryonic brain by RT-PCR with specific primers. The invention related the methods of using the protein and DNA for treatment of various diseases, such as mitochondrial myopathy, neurodegenerative disorder, immune disorder, and malignant tumors. The invention provides methods, expression vectors, host cells for recombinant prodn. of the protein, and antibody against the protein.

L26 ANSWER 64 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:107553 CAPLUS <<LOGINID::20080906>>
DN 136:146225
TI Human translocase of the inner mitochondrial membrane TIM23 sequence homolog 11.66 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Shanghai Biowindow Gene Development Inc., Peop. Rep. China
SO PCT Int. Appl., 37 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2002010397 A1 20020207 WO 2001-CN1077 20010629 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1331297 A 20020116 CN 2000-116939 20000630 AU 2002014915 A 20020213 AU 2002-14915 20010629
PRAI CN 2000-116939 A 20000630 WO 2001-CN1077 W 20010629
AB The invention provides cDNA sequences of a novel human translocase of the inner mitochondrial membrane TIM23 sequence homolog 11.66 (named by protein MW detected in SDS-PAGE gel) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E. coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. The mRNA expression profile in various normal or tumor cell lines and tissues is also provided. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 65 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2002:50601 CAPLUS <<LOGINID::20080906>>
DN 137:120188
TI Large mitochondrial repeats multiplied during the polymerase chain reaction
AU Campbell, Nick J. H.; Sturm, Richard A.; Barker, Stephen C.
CS Department of Microbiology and Parasitology, The University of Queensland, Brisbane, Q 4072, Australia
SO Molecular Ecology Notes (2001), 1(4), 336-340 CODEN: MENOCX; ISSN: 1471-8278
PB Blackwell Science Ltd.
DT Journal
LA English
AB The no. of repeats in repetitive DNA like micro- and minisatellites is often detd. by polymerase chain reaction (PCR). When we counted repeats in an ***array*** of ***mitochondrial*** repeats in the cattle tick (Boophilus microplus) we found that the no. of repeats increased during PCR. Multiplication of the repeats was independent of the primers used to amplify the region, the PCR annealing temp. and the length of the PCR product. The use of PCR to det. the no. of repeats in arrays needs to be reassessed. For long repeats, a subset of samples should always be analyzed by Southern blot hybridization to confirm the PCR results.
RE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 66 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:870002 CAPLUS <<LOGINID::20080906>>
DN 136:1658
TI Human mitochondrial carrier protein 14 hMCP14 and its cDNA and therapeutic use thereof
IN Mao, Yumin; Xie, Yi; Qiu, Minyan; Wang, Yong; Jiang, Guangping
PA Borong Gene Development Co., Ltd., Shanghai, Peop. Rep. China

SO Faming Zhuanli Shenqing Gongkai Shuomingshu, 31 pp.
CODEN: CNXXEV
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI CN 1297937 A 20010606 CN 1999-124166 19991130
PRAI CN 1999-124166 19991130
AB The invention provides cDNA sequences of a novel human mitochondrial carrier protein 14 hMCP14 (14 kDa) cloned from human embryonic brain. The invention also relates to constructing the cloned gene expression vectors to prep. its recombinant protein using E.coli cells or eukaryotic cells. Methods of expressing and prepg. the above recombinant protein and its antibody are described. Methods of using related gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed. Methods for screening for related analogs, agonists, inhibitors and antagonists to be used as therapeutic drugs are also described.

L26 ANSWER 67 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:834885 CAPLUS <<LOGINID::20080906>>
DN 136:80805
TI Mitochondrial inheritance in Schistosoma mansoni: mitochondrial variable number tandem repeat mutation produces noise on top of the signal
AU Bieberich, Andrew A.; Minchella, Dennis J.
CS Department of Biological Sciences, Purdue University, West Lafayette, IN, 47907, USA
SO Journal of Parasitology (2001), 87(5), 1011-1015 CODEN: JOPAA2; ISSN: 0022-3395
PB American Society of Parasitologists
DT Journal
LA English
AB The Schistosoma mansoni ***mitochondrial*** genome contains tandemly ***arrayed*** copies of a 62-base repeat motif. The tandem array is highly polymorphic with respect to no. of repeats and commonly exhibits heteroplasmy. This study shows that a very high rate of mutation rapidly produces new repeat lengths (new haplotypes) for this mitochondrial variable no. tandem repeat. A maternal inheritance pattern is also demonstrated for this repeat sequence, while the high mutation rate causes some offspring to exhibit nonmaternal haplotypes. Frequent generation of new haplotypes can be obsd. within samples of clonal cohorts taken from monomiracidial snail infections. These same clonal cercarial groups, when crossed, produce F1 generations that exhibit the maternal set of haplotypes, across all individuals, with the frequent addn. of new mutant haplotypes. In each of 2 crosses, a subset of the recently arisen haplotypes match paternal haplotypes by chance (30.4% and 18.8%), thus giving the false appearance of partial paternal inheritance of mitochondria.
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 68 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:730806 CAPLUS <<LOGINID::20080906>>
DN 135:284022
TI Protein and cDNA sequences of 14 kDa human mitochondrial ATPase coupling factor-like protein and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Shanghai Biowindow Gene Development Inc., Peop. Rep. China
SO PCT Int. Appl., 33 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2001072813 A1 20011004 WO 2001-CN480 20010326 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1315396 A 20011003 CN 2000-115195 20000328 AU 2001063718 A 20011008 AU 2001-63718 20010326
PRAI CN 2000-115195 A 20000328 WO 2001-CN480 W 20010326
AB The invention provides protein and cDNA sequences for 14 kDa novel human protein cloned from fetal brain, and which have similar expression pattern with human mitochondrial ATPase coupling factor 10. The invention also relates to constructing mitochondrial ATPase coupling factor-like protein gene expression vectors to prep. recombinant mitochondrial ATPase coupling factor-like protein using prokaryote or eukaryote cells. Methods of expressing and prepg. recombinant mitochondrial ATPase coupling factor-like protein and its antibody are described. Methods of using mitochondrial ATPase coupling factor-like protein gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed.
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 69 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:715008 CAPLUS <<LOGINID::20080906>>
DN 136:162468
TI Microarray Analysis of Differential Gene Expression in Lead-Exposed Astrocytes
AU Bouton, Christopher M. L. S.; Hossain, Mir Ahamed; Frelin, Laurence P.; Laterra, John; Pevsner, Jonathan
CS Department of Neuroscience, Johns Hopkins University, Baltimore, MD, 21205, USA
SO Toxicology and Applied Pharmacology (2001), 176(1), 34-53 CODEN: TXAPA9; ISSN: 0041-008X
PB Academic Press
DT Journal
LA English
AB The toxic metal lead is a widespread environmental health hazard that can adversely affect human health. In an effort to better understand the cellular and mol. consequences of lead exposure, we have employed cDNA microarrays to analyze the effects of acute lead exposure on large-scale gene expression patterns in immortalized rat astrocytes. Our studies identified many genes previously reported to be differentially regulated by lead exposure. Addnl., we have identified novel putative targets of lead-mediated toxicity, including members of the family of calcium/phospholipid binding annexins, the angiogenesis-inducing

thrombospondins, collagens, and tRNA synthetases. We demonstrate the ability to distinguish lead-exposed samples from control or sodium samples solely on the basis of large-scale gene expression patterns using two complementary clustering methods. We have confirmed the altered expression of candidate genes and their encoded proteins by RT-PCR and Western blotting, resp. Finally, we show that the calcium-dependent phospholipid binding protein annexin A5, initially identified as a differentially regulated gene by our microarray anal., is directly bound and activated by nanomolar concns. of lead. We conclude that microarray technol. is an effective tool for the identification of lead-induced patterns of gene expression and mol. targets of lead. (c) 2001 Academic Press.
RE.CNT 151 THERE ARE 151 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 70 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:713400 CAPLUS <<LOGINID::20080906>>
DN 135:268287
TI A human 9 kilodalton mitochondrial carrier protein, protein and cDNA sequences, tissue distribution, recombinant production and therapeutic uses
IN Mao, Yumin; Xie, Yi
PA Shanghai Biowindow Gene Development Inc., Peop. Rep. China
SO PCT Int. Appl., 36 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001070793 A1 20010927 WO 2001-CN399 20010323 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1315346 A 20011003 CN 2000-115088 20000324 AU 2001081491 A 20011003 AU 2001-81491 20010323
PRAI CN 2000-115088 A 20000324 WO 2001-CN399 W 20010323
AB The invention relates to a human mitochondrial carrier protein. The open reading frame of the cDNA encodes 80 amino acids and the mol. wt. of the protein was estd. to be 9 kilodalton on SDS-PAGE. The invention provides the method of applying the polypeptide or polynucleotide for treatment of various kinds of diseases, such as cancer, blood disease, HIV infection, immune diseases and inflammation. The invention also relates to methods, expression vectors and host cells for recombinant prodn. of said mitochondrial carrier protein. The invention also relates to agonist and antagonist of said mitochondrial carrier protein and uses in therapy. The tissue expression profile of said mitochondrial carrier protein is similar to that of human 14 kilodalton mitochondrial carrier protein.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 71 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:697273 CAPLUS <<LOGINID::20080906>>
DN 136:148347
TI High-density DNA microarray membranes to study gene expression patterns associated with human airway epithelial cell differentiation in culture
AU Chang, Mary M. J.; Chen, Yin; Zhao, Yu Hua; Wu, Reen; Li, Ching; Peck, Konan
CS University of California, Davis, CA, USA
SO Cilia and Mucus: From Development to Respiratory Defense, [International Meeting], 2nd, Sirmione, Italy, Nov. 3-4, 1999 (2001), Meeting Date 1999, 225-237. Editor(s): Salathe, Matthias. Publisher: Marcel Dekker, Inc., New York, N. Y. CODEN: 69BVC5
DT Conference
LA English
AB The purpose of this paper is to utilize the newly developed technol. of microarray membranes to analyze genes whose expression is assocd. with mucociliary differentiation of human airway epithelial cells in vivo. Two types of nylon membranes were used. One contains 884 sequence-verified expression sequence tag (EST) clones, the other contains 576-uni EST clones. Data obtained from these membranes were further characterized by Northern blot hybridization.
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 72 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:563002 CAPLUS <<LOGINID::20080906>>
DN 136:350488
TI Effect of a herbal protein CI-1, purified from Cajanus indicus on the ultrastructural study of hepatocytes, in models of liver failure in mice
AU Datta, S.; Bhattacharyya, P.
CS Bose Institute, Calcutta, West Bengal, 700009, India
SO Journal of Ethnopharmacology (2001), 77(1), 11-18 CODEN: JOETD7; ISSN: 0378-8741
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB Ultrastructural changes in acute liver damage models in swiss albino mice (male, 30 g .+-.2) induced by CCl4 (0.1 mL/100 g); .beta.-galactosamine (500 mg/kg); paracetamol (300-500 mg/kg) and 40% ethanol (2 mL/100 g) were studied. Electron microscopical studies of hepatocytes of treated (hepatotoxins) mice showed-dilation of ER of both rough and smooth type with swollen mitochondria. Ethanol treated mouse hepatocytes showed giant mitochondria and presence of balloon cells. Nuclear changes showed increase in size and striking anisonucleosis, esp. in CCl4 and paracetamol treated mouse hepatocytes. Condensation of chromatin, nucleoli were fragmented and dispersed in .beta.-galactosamine induced hepatotoxic mice. These changes are remarkably striking in contrast to control animals. Treatment with CI-1, the herbal protein isolated from Cajanus indicus inhibited the pathogenesis of a majority of lesions produced by the hepatotoxins. Slender ***mitochondria*** , ***array*** of granular ER, presence of binucleated cells are the salient features of CI-1 treated hepatotoxic mice. Ultrastructurally, the hepatocytes of CI-1 treated mice were near normal. Thus, the herbal protein CI-1, may be a useful approach in the treatment of liver disorders for its potential in clin. medicine.

RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 73 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:489451 CAPLUS <<LOGINID::20080906>>
DN 135:103382
TI Protein and cDNA of a human mitochondrial carrier 30 and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bioroad Gene Development Ltd. Shanghai, Peop. Rep. China
SO PCT Int. Appl., 33 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001047982 A1 20010705 WO 2000-CN516 20001127 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CN 1297895 A 20010606 CN 1999-124165 19991130
PRAI CN 1999-124165 A 19991130
AB The invention provides cDNA sequences for a novel human mitochondrial carrier 30 cloned from placenta brain, and its protein sequences which have sequence homol. to the structural domain of a mitochondrial transport protein. The invention also relates to constructing mitochondrial carrier 30 gene expression vectors to prep. recombinant mitochondrial carrier 30 protein using prokaryote or eukaryote cells. Methods of expressing and prepg. recombinant mitochondrial carrier 30 protein and its antibody are described. Methods of using mitochondrial carrier 30 gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed.
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 74 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:473659 CAPLUS <<LOGINID::20080906>>
DN 135:205729
TI Microarray analysis of the in vivo effects of hypophysectomy and growth hormone treatment on gene expression in the rat
AU Flores-Morales, Amilcar; Stahlberg, Nina; Tollet-Egnell, Petra; Lundeberg, Joakim; Malek, Renae L.; Quackenbush, John; Lee, Norman H.; Norstedt, Gunnar
CS Department of Molecular Medicine, Karolinska Institute, Stockholm, 17176, Swed.
SO Endocrinology (2001), 142(7), 3163-3176 CODEN: ENDOAO; ISSN: 0013-7227
PB Endocrine Society
DT Journal
LA English
AB The authors used cDNA microarrays contg. 3000 different rat genes to study the consequences of severe hormonal deficiency (hypophysectomy) on the gene expression patterns in heart, liver, and kidney. Hybridization signals were seen from a majority of the arrayed cDNAs; nonetheless, tissue-specific expression patterns could be delineated. Hypophysectomy affected the expression of genes involved in a variety of cellular functions. Between 16-29% of the detected transcripts from each tissue changed expression level as a reaction to this condition. Chronic treatment of hypophysectomized animals with human GH also caused significant changes in gene expression patterns. The study confirms previous knowledge concerning certain gene expression changes in the above-mentioned situations and provides new information regarding hypophysectomy and chronic human GH effects in the rat. Furthermore, the authors have identified several new genes that respond to GH treatment. The results represent a first step toward a more global understanding of gene expression changes in states of hormonal deficiency.
RE.CNT 92 THERE ARE 92 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 75 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:434529 CAPLUS <<LOGINID::20080906>>
DN 136:80393
TI Numerical methods for handling uncertainty in ***microarray*** data: an example analyzing perturbed ***mitochondrial*** function in yeast
AU Epstein, Charles B.; Hale, Walker, IV; Butow, Ronald A.
CS Department of Molecular Biology, University of Texas Southwestern Medical Center, Dallas, TX, 75390, USA
SO Methods in Cell Biology (2001), 65(Mitochondria), 439-452 CODEN: MCBLAG; ISSN: 0091-679X
PB Academic Press
DT Journal; General Review
LA English
AB A review discusses the methodol. issues related to the processing and evaluation of numerical results from microarray expts. The application of ***microarray*** technol. to the study the effect of perturbation of ***mitochondrial*** function in gene expression in yeast is described. The quant. methods in microarray includes the radiometric method, image acquisition, image processing and data anal., and variability in microarray data. (c) 2001 Academic Press.
RE.CNT 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 76 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:416997 CAPLUS <<LOGINID::20080906>>
DN 135:41809
TI Protein and cDNA of a human mitochondrial carrier 12 and therapeutic use thereof
IN Mao, Yumin; Xie, Yi
PA Bioroad Gene Development Ltd. Shanghai, Peop. Rep. China
SO PCT Int. Appl., 37 pp. CODEN: PIXXD2
DT Patent
LA Chinese
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001040289 A1 20010607 WO 2000-CN518 20001127 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK,

MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI CN 1999-124163 A 19991130
AB The invention provides cDNA sequences for a novel human mitochondrial carrier 12 cloned from placenta brain, and its protein sequences which have sequence homol. to the structural domain of a mitochondrial transport protein. The invention also relates to constructing mitochondrial carrier 12 gene expression vectors to prep. recombinant mitochondrial carrier 12 protein using prokaryote or eukaryote cells. Methods of expressing and prepg. recombinant mitochondrial carrier 12 protein and its antibody are described. Methods of using mitochondrial carrier 12 gene or protein products for the treatment of various kinds of diseases, such as cancer, blood diseases, HIV infection, immune diseases and inflammation are also disclosed.
RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 77 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:353570 CAPLUS <<LOGINID::20080906>>
DN 136:97095
TI Nuclear gene dosage effects upon the expression of maize mitochondrial genes
AU Auger, Donald L.; Newton, Kathleen J.; Birchler, James A.
CS Division of Biological Sciences, University of Missouri, Columbia, MO, 65211, USA
SO Genetics (2001), 157(4), 1711-1721 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB Each mitochondrion possesses a genome that encodes some of its own components. The nucleus encodes most of the mitochondrial proteins, including the polymerases and factors that regulate the expression of mitochondrial genes. Little is known about the no. or location of these nuclear factors. B-A translocations were used to create dosage series for 14 different chromosome arms in maize plants with normal cytoplasm. The presence of one or more regulatory factors on a chromosome arm was indicated when variation of its dosage resulted in the alteration in the amt. of a mitochondrial transcript. We used quant. Northern anal. to assay the transcript levels of three mitochondrially encoded components of the cytochrome c. oxidase complex (cox1, cox2, and cox3). Data for a nuclearly encoded component (cox5b) and for two mitochondrial genes that are unrelated to cytochrome c oxidase, ATP synthase .alpha.-subunit and 18S rRNA, were also detd. Two tissues, embryo and endosperm, were compared and most effects were found to be tissue specific. Significantly, the ***array*** of dosage effects upon ***mitochondrial*** genes was similar to what had been previously found for nuclear genes. These results support the concept that although mitochondrial genes are prokaryotic in origin, their regulation has been extensively integrated into the eukaryotic cell.
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 78 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:315173 CAPLUS <<LOGINID::20080906>>
DN 135:120665
TI Lack of dystrophin is associated with altered integration of the mitochondria and ATPases in slow-twitch muscle cells of MDX mice
AU Braun, U.; Paju, K.; Eimre, M.; Seppet, E.; Orlova, E.; Kadaja, L.; Trumbeckaite, S.; Gellerich, F. N.; Zierz, S.; Jockusch, H.; Seppet, E. K.
CS Department of Pathophysiology, Faculty of Medicine, University of Tartu, Tartu, 50411, Estonia
SO Biochimica et Biophysica Acta, Bioenergetics (2001), 1505(2-3), 258-270 CODEN: BBBEB4; ISSN: 0005-2728
PB Elsevier B.V.
DT Journal
LA English
AB The potential role of dystrophin-mediated control of systems integrating mitochondria with ATPases was assessed in muscle cells. Mitochondrial distribution and function in skinned cardiac and skeletal muscle fibers from dystrophin-deficient (MDX) and wild-type mice were compared. Laser confocal microscopy revealed disorganized ***mitochondrial*** ***arrays*** in m. gastrocnemius in MDX mice, whereas the other muscles appeared normal in this group. Irresp. of muscle type, the absence of dystrophin had no effect on the maximal capacity of oxidative phosphorylation, nor on coupling between oxidn. and phosphorylation. However, in the myocardium and m. soleus, the coupling of mitochondrial creatine kinase to adenine nucleotide translocase was attenuated as evidenced by the decreased effect of creatine on the Km for ADP in the reactions of oxidative phosphorylation. In m. soleus, a low Km for ADP compared to the wild-type counterpart was found, which implies increased permeability for that nucleotide across the mitochondrial outer membrane. In normal cardiac fibers 35% of the ADP flux generated by ATPases was not accessible to the external pyruvate kinase-phosphoenolpyruvate system, which suggests the compartmentalized (direct) channeling of that fraction of ADP to mitochondria. Compared to control, the direct ADP transfer was increased in MDX ventricles. In conclusion, our data indicate that in slow-twitch muscle cells, the absence of dystrophin is assocd. with the rearrangement of the intracellular energy and feedback signal transfer systems between mitochondria and ATPases. As the mechanisms mediated by creatine kinases become ineffective, the role of diffusion of adenine nucleotides increases due to the higher permeability of the mitochondrial outer membrane for ADP and enhanced compartmentalization of ADP flux.
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 79 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:312024 CAPLUS <<LOGINID::20080906>>
DN 135:340138
TI A genome approach to mitochondrial-nuclear communication in Arabidopsis
AU Yu, Jianping; Nickels, Roxy; McIntosh, Lee
CS MSU-DOE Plant Research Laboratory, Michigan State University, East Lansing, MI, 48824, USA
SO Plant Physiology and Biochemistry (Paris, France) (2001), 39(3-4), 345-353 CODEN: PPBIEX; ISSN: 0981-9428
PB Editions Scientifiques et Medicales Elsevier
DT Journal
LA English
AB Mitochondria depend on the nuclear genome to encode the vast majority of their proteins; in turn they control the expression

of certain nuclear genes to maintain proper functioning. In this work, Arabidopsis leaves were employed as a model to study nuclear gene expression in response to inhibition of the mitochondrial electron transport by antimycin A. Microarrays contg. 11 514 Arabidopsis expressed sequence tags supplied through the Arabidopsis Functional Genomics Consortium (AFGC) were used. Transcript levels of 579 nuclear genes were increased .gtoreq. 2-fold, and the levels of 584 nuclear genes were decreased .gtoreq. 2-fold after antimycin A treatment. While functions of a large no. of the gene products are unknown, others are involved in diverse metabolic activities such as phosphorylation, transcription, and energy metab. Data from microarray expts. were repeatable and were confirmed by northern hybridization for specific test genes. It was found through cluster anal. that plant cells show significant common response to chem. inhibition of mitochondrial function, aluminum stress, cadmium stress, hydrogen peroxide and virus infection. The results imply that these stresses may act on mitochondria and the responses are in part mediated by mitochondrial-nuclear communication. Most nuclear-encoded respiratory genes involved in the TCA cycle, electron transport and ATP synthesis did not respond to signals from the inhibited mitochondria, while genes for cytochrome c and alternative oxidase were induced. The result indicates that these two genes may be targets in the transcriptional regulation of the two respiratory pathways.
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 80 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:295103 CAPLUS <<LOGINID::20080906>>
DN 136:1249
TI Detection of ***mitochondrial*** single nucleotide polymorphisms using a primer elongation reaction on oligonucleotide ***microarrays***
AU Erdogan, Fikret; Kirchner, Roland; Mann, Wolfgang; Ropers, Hans-Hilger; Nuber, Ulrike A.
CS Max-Planck Institute for Molecular Genetics, Berlin, 14195, Germany
SO Nucleic Acids Research (2001), 29(7), e36/1-e36/7 CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The authors have developed a novel allele-specific primer elongation protocol using a DNA polymerase on oligonucleotide chips. Oligonucleotide primers carrying polymorphic sites at their free 3'end were covalently bound to glass slides. The generation of single-stranded targets of genomic DNA contg. single nucleotide polymorphisms (SNPs) to be typed was achieved by an asym. PCR reaction or exonuclease treatment of phosphothioate (PTO)-modified PCR products. In the presence of DNA polymerase and all four dNTPs, with Cy3-dUTP replacing dTTP, allele-specific extension of the immobilized primers took place along a stretch of target DNA sequence. The yield of elongated products was increased by repeated reaction cycles. The authors performed multiplexed assays with many small DNA targets, or used single targets of up to 4.4 kb mitochondrial DNA (mtDNA) sequence to detect multiple SNPs in one reaction. The latter approach greatly simplifies preamplification of SNP-contg. regions, thereby providing a framework for typing hundreds of mtDNA polymorphisms.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 81 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:292835 CAPLUS <<LOGINID::20080906>>
DN 135:30042
TI Aluminum toxicity studies in Vaucheria longicaulis var. macounii (Xanthophyta, Tribophyceae). II. Effects on the F-actin array
AU Alessa, L.; Oliveira, L.
CS Department of Biology, University of Alaska, Anchorage, AK, 99508, USA
SO Environmental and Experimental Botany (2001), 45(3), 223-237 CODEN: EEBODM; ISSN: 0098-8472
PB Elsevier Science B.V.
DT Journal
LA English
AB In this study, the authors test the hypothesis that exposure to environmentally significant concns. of Al, 80 .mu.M causes the microfilament array of Vaucheria longicaulis var. macounii vegetative filaments to become fragmented and disorganized. Changes in F-actin organization following treatment of vegetative filaments by Al are examd. using vital staining with fluorescein phalloidin. In the cortical cytoplasm of the apical zone of pH 7.5 and pH 4.5 control cells, axially aligned bundles of F-actin lead to a region of diffuse, brightly stained material. Dimly stained focal masses are noted deeper in the cytoplasm of the apical zone whereas they are absent from the zone of vacuolation. The F-actin array is visualized in the cortical cytoplasm of the region of the cell, distal to the apical tip, which exhibits vigorous cytoplasmic streaming (zone of vacuolation) as long, axially aligned bundles with which chloroplasts and mitochondria assoc. Thirty minutes following treatment with aluminum, and for the next 8-16 h, the F-actin array is progressively disorganized. The longitudinally aligned F-actin array becomes fragmented. Aggregates of F-actin, such as short rods, amorphous and stellate F-actin focal masses, curved F-actin bundles and F-actin rings replace the control array. Each of these structures may occur in assocn. with chloroplasts or independently with no apparent assocn. with organelles. Images are recorded which indicate that F-actin rings not assocd. with organelles may self-assemble by successive bundling of F-actin fragments. The fragmentation and bundling of F-actin in cells of V. longicaulis upon treatment with aluminum resembles those reported after diverse forms of cell disturbance and supports the hypothesis that aluminum-induced changes in the F-actin array may be a calcium-mediated response to stress.
RE.CNT 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 82 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:216268 CAPLUS <<LOGINID::20080906>>
DN 135:299332
TI Mitochondrial control of iron homeostasis. A genome wide analysis of gene expression in a yeast frataxin-deficient strain
AU Foury, Francoise; Talibi, Driss
CS Unite de Biochimie Physiologique, Louvain-la-Neuve, 1348, Belg.
SO Journal of Biological Chemistry (2001), 276(11), 7762-7768 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Deletion of YFH1, the yeast frataxin homolog gene, elicits mitochondrial iron accumulation and alters cellular iron

homeostasis. Here, we report a genome wide anal. of gene expression in a yfh1(.DELTA.YFH1) deleted strain. Frataxin deficiency results in enhanced expression of some 70 genes including a set of genes, called the iron regulon, that are under the control of the iron-sensing transcription factor AFT1. Five new AFT1-dependent genes, YOR382w, YOR383c, YDR534c, YLR136c, and YLR205c were found. The first three genes presumably encode cell-wall glycosylphosphatidylinositol anchor proteins and exhibit a 30-100-fold increased expression. The triple deletion of these genes decreases efficiency in utilization of the iron of ferrioxamine B by the yeast cell. YLR136c bears homol. to tristetraproline proteins, which are post-transcriptional regulators in mammalian cells. Deletion of YLR136c increases the mRNA levels of iron regulon members. YLR205c bears homol. to heme oxygenases. Our data show that frataxin deficiency elicits iron mobilization from all iron sources in an AFT1-dependent manner. Wild-type and .DELTA.YFH1 glycerol-grown cells exhibit similar high respiration rates, no mitochondrial iron accumulation, and high expression of the iron regulon, suggesting that under these conditions little iron is extruded from mitochondria. These data suggest that the activity of Yfh1p is not essential in cells grown on glycerol. This study has also revealed unexpected links between mitochondria and remote metabolic pathways since frataxin deficiency also enhances the expression of genes such as HSP30, that escape to AFT1 control. Finally, no oxidative stress gene is induced.
RE.CNT 52 THERE ARE 52 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 83 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2001:135064 CAPLUS <<LOGINID::20080906>>
DN 134:306739
TI Genome-wide responses to mitochondrial dysfunction
AU Epstein, Charles B.; Waddle, James A.; Hale, Walker, IV; Dave, Varshal; Thornton, Janet; Macatee, Timothy L.; Garner, Harold R.; Butow, Ronald A.
CS Department of Molecular Biology, University of Texas Southwestern Medical Center, Dallas, TX, 75390-9148, USA
SO Molecular Biology of the Cell (2001), 12(2), 297-308 CODEN: MBCEEV; ISSN: 1059-1524
PB American Society for Cell Biology
DT Journal
LA English
AB Mitochondrial dysfunction can lead to diverse cellular and organismal responses. We used DNA ***microarrays*** to characterize the transcriptional responses to different ***mitochondrial*** perturbations in Saccharomyces cerevisiae. We examd. respiratory- deficient petite cells and respiratory-competent wild-type cells treated with the inhibitors of oxidative phosphorylation antimycin, carbonyl cyanide m-chlorophenylhydrazone, or oligomycin. We show that respiratory deficiency, but not inhibition of mitochondrial ATP synthesis per se, induces a suite of genes assocd. with both peroxisomal activities and metabolite-restoration (anaplerotic) pathways that would mitigate the loss of a complete tricarboxylic acid cycle. The array data suggested, and direct microscopic observation of cells expressing a deriv. of green fluorescent protein with a peroxisomal matrix-targeting signal confirmed, that respiratory deficiency dramatically induces peroxisome biogenesis. Transcript profiling of cells harboring null alleles of RTG1, RTG2, or RTG3, genes known to control signaling from mitochondria to the nucleus, suggests that there are multiple pathways of cross-talk between these organelles in yeast.
RE.CNT 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 84 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:882002 CAPLUS <<LOGINID::20080906>>
DN 134:143335
TI Mitochondria as all-round players of the calcium game
AU Rizzuto, Rosario; Bernardi, Paolo; Pozzan, Tullio
CS Department of Experimental and Diagnostic Medicine, Section of General Pathology, University of Ferrara, Italy
SO Journal of Physiology (Cambridge, United Kingdom) (2000), 529(1), 37-47 CODEN: JPHYA7; ISSN: 0022-3751
PB Cambridge University Press
DT Journal; General Review
LA English
AB A review, with 64 refs. Although it has been known for >3 decades that ***mitochondria*** are endowed with a complex ***array*** of Ca2+ transporters and that key enzymes of ***mitochondrial*** metab. are regulated by Ca2+, the possibility that physiol. stimuli that raise the [Ca2+] of the cytoplasm could trigger major mitochondrial Ca2+ uptake has long been considered unlikely, based on the low affinity of the mitochondrial transporters and the limited amplitude of the cytoplasmic [Ca2+] rises. The direct measurement of mitochondrial [Ca2+] with highly selective probes has led to a complete reversion of this view, by demonstrating that, after cell stimulation, the cytoplasmic Ca2+ signal is always paralleled by a much larger rise in [Ca2+] in the mitochondrial matrix. This observation has rejuvenated the study of mitochondrial Ca2+ transport and novel, unexpected results have altered long-standing dogmas in the field of calcium signaling. Here we focus on 4 main topics: (1) the current knowledge of the functional properties of the Ca2+ transporters and of the thermodn. constraints under which they operate; (2) the occurrence of mitochondrial Ca2+ uptake in living cells and the key role of local signaling routes between the mitochondria and the Ca2+ sources; (3) the physiol. consequences of Ca2+ transport for both mitochondrial function and the modulation of the cytoplasmic Ca2+ signal; and (4) evidence that alterations of mitochondrial Ca2+ signaling may occur in pathophysiol. conditions.
RE.CNT 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 85 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:870510 CAPLUS <<LOGINID::20080906>>
DN 135:4019
TI Human Cu/Zn Superoxide Dismutase (SOD1) Overexpression in Mice Causes Mitochondrial Vacuolization, Axonal Degeneration, and Premature Motoneuron Death and Accelerates Motoneuron Disease in Mice Expressing a Familial Amyotrophic Lateral Sclerosis Mutant SOD1
AU Jaarsma, Dick; Haasdijk, Elize D.; Grashorn, J. A. C.; Hawkins, Richard; van Duijn, Wim; Verspaget, Hein W.; London, Jacqueline; Holstege, Jan C.
CS Department of Anatomy, Erasmus University, Rotterdam, Neth.
SO Neurobiology of Disease (2000), 7(6), 623-643 CODEN: NUDIEM; ISSN: 0969-9961
PB Academic Press
DT Journal
LA English

AB Cytosolic Cu/Zn superoxide dismutase (SOD1) is a ubiquitous small cytosolic metalloenzyme that catalyzes the conversion of superoxide anion to hydrogen peroxide (H2O2). Mutations in the SOD1 gene cause a familial form of amyotrophic lateral sclerosis (fALS). The mechanism by which mutant SOD1s causes ALS is not understood. Transgenic mice expressing multiple copies of fALS-mutant SOD1s develop an ALS-like motoneuron disease resembling ALS. Here we report that transgenic mice expressing a high concn. of wild-type human SOD1 (hSOD1WT) develop an ***array*** of neurodegenerative changes consisting of (1) swelling and vacuolization of ***mitochondria*** , predominantly in axons in the spinal cord, brain stem, and subiculum; (2) axonal degeneration in a no. of long fiber tracts, predominantly the spinocerebellar tracts; and (3) at 2 yr of age, a moderate loss of spinal motoneurons. Parallel to the development of neurodegenerative changes, hSOD1WT mice also develop mild motor abnormalities. Interestingly, mitochondrial vacuolization was assocd. with accumulation of hSOD1 immunoreactivity, suggesting that the development of mitochondrial pathol. is assocd. with disturbed SOD1 turnover. In this study we also crossed hSOD1WT mice with a line of fALS-mutant SOD1 mice (hSOD1G93A) to generate "double" transgenic mice that express high levels of both wild-type and G93A mutant hSOD1. The "double" transgenic mice show accelerated motoneuron death, earlier onset of paresis, and earlier death as compared with hSOD1G93A littermates. Thus in vivo expression of high levels of wild-type hSOD1 is not only harmful to neurons in itself, but also increases or facilitates the deleterious action of a fALS-mutant SOD1. Our data indicate that it is important for motoneurons to control the SOD1 concn. throughout their processes, and that events that lead to improper synthesis, transport, or breakdown of SOD1 causing its accumulation are potentially dangerous. (c) 2000 Academic Press.
RE.CNT 69 THERE ARE 69 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 86 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:763360 CAPLUS <<LOGINID::20080906>>
DN 134:3163
TI Treadmill running produces both positive and negative physiological adaptations in Sprague-Dawley rats
AU Moraska, Albert; Deak, Terrence; Spencer, Robert L.; Roth, David; Fleshner, Monika
CS Departments of Kinesiology and Applied Physiology, University of Colorado, Boulder, CO, 80309, USA
SO American Journal of Physiology (2000), 279(4, Pt. 2), R1321-R1329 CODEN: AJPHAP; ISSN: 0002-9513
PB American Physiological Society
DT Journal
LA English
AB Exercise training produces a vast ***array*** of physiol. adaptations, ranging from changes in metab. to muscle ***mitochondrial*** biogenesis. Researchers studying the physiol. effects of exercise often use animal models that employ forced exercise regimens that include aversive motivation, which could activate the stress response. This study examd. the effect of forced treadmill running (8 wk) on several physiol. systems that are sensitive to training and stress. Forced treadmill running produced both pos. and neg. physiol. adaptations. Indicative of pos. training adaptations, exercised male Sprague-Dawley rats had a decrease in body wt. gain and an increase in muscle citrate synthase activity compared with sedentary controls. In contrast, treadmill running also resulted in the potentially neg. adaptations of adrenal hypertrophy, thymic involution, decreased serum corticosteroid binding globulin, elevated lymphocyte nitrite concns., suppressed lymphocyte proliferation, and suppressed antigen-specific IgM. Such alterations in neuroendocrine tissues and immune responses are commonly assocd. with chronic stress. Thus treadmill running produces both pos. training adaptations and potentially neg. adaptations that are indicative of chronic stress. Researchers employing forced activity need to be aware that this type of exercise procedure also produces physiol. adaptations indicative of chronic stress and that these changes could potentially impact other measures of interest.
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 87 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:445329 CAPLUS <<LOGINID::20080906>>
DN 134:203246
TI Tandemly repeated sequences in mtDNA control region of whitefish, Coregonus lavaretus
AU Brzuzan, Pawel
CS Department of Evolutionary Ecology, WM University of Olsztyn, Olsztyn, 10-957, Pol.
SO Genome (2000), 43(3), 584-587 CODEN: GENOE3; ISSN: 0831-2796
PB National Research Council of Canada
DT Journal
LA English
AB Length variation of the mitochondrial DNA control region was obsd. with PCR amplification of a sample of 138 whitefish (Coregonus lavaretus). Nucleotide sequences of representative PCR products showed that the variation was due to the presence of an approx. 100-bp motif tandemly repeated two, three, or five times in the region between the conserved sequence block-3 (CSB-3) and the gene for phenylalanine tRNA. This is the first report on the tandem ***array*** composed of long repeat units in ***mitochondrial*** DNA of salmonids.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 88 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:202208 CAPLUS <<LOGINID::20080906>>
DN 133:54238
TI Gene ***microarray*** identification of redox and ***mitochondrial*** elements that control resistance or sensitivity to apoptosis
AU Voehringer, D. W.; Hirschberg, D. L.; Xiao, J.; Lu, Q.; Roederer, M.; Lock, C. B.; Herzenberg, L. A.; Steinman, L.; Herzenberg, L. A.
CS Department of Genetics, Stanford University School of Medicine, Stanford, CA, 94305, USA
SO Proceedings of the National Academy of Sciences of the United States of America (2000), 97(6), 2680-2685 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Multigenic programs controlling susceptibility to apoptosis in response to ionizing radiation have not yet been defined. Here, using DNA microarrays, we show gene expression patterns in an apoptosis-sensitive and apoptosis-resistant murine B cell lymphoma model system both before and after irradn. From the 11,000 genes interrogated by the arrays, two major patterns

emerged. First, before radiation exposure the radioresistant LYar cells expressed significantly greater levels of message for several genes involved in regulating intracellular redox potential. Compared with LYas cells, LYar cells express 20- to 50-fold more mRNA for the tetraspanin CD53 and for fructose-1,6-bisphosphatase. Expression of both of these genes can lead to the increase of total cellular glutathione, which is the principle intracellular antioxidant and has been shown to inhibit many forms of apoptosis. A second pattern emerged after radiation, when the apoptosis-sensitive LYas cells induced rapid expression of a unique cluster of genes characterized by their involvement in mitochondrial electron transport. Some of these genes have been previously recognized as proapoptotic; however others, such as uncoupling protein 2, were not previously known to be apoptotic regulatory proteins. From these observations we propose that a multigenic program for sensitivity to apoptosis involves induction of transcripts for genes participating in mitochondrial uncoupling and loss of membrane potential. This program triggers mitochondrial release of apoptogenic factors and induces the "caspase cascade". Conversely, cells resistant to apoptosis down-regulate these biochem. pathways, while activating pathways for establishment and maintenance of high intracellular redox potential by means of elevated glutathione.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 89 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 2000:41442 CAPLUS <<LOGINID::20080906>>
DN 132:177386
TI A novel human nucleoside diphosphate (NDP) kinase, Nm23-H6, localizes in mitochondria and affects cytokinesis
AU Tsuiki, Hiromasa; Nitta, Masayuki; Furuya, Akiko; Hanai, Nobuo; Fujiwara, Toshiyoshi; Inagaki, Masaki; Kochi, Masato; Ushio, Yukitaka; Saya, Hideyuki; Nakamura, Hideo
CS Department of Tumor Genetics and Biology, Kumamoto University School of Medicine, Kumamoto, 860-0811, Japan
SO Journal of Cellular Biochemistry (1999), Volume Date 2000, 76(2), 254-269 CODEN: JCEBD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Nucleoside diphosphate kinases (NDP kinases) are enzymes known to be conserved throughout evolution and have been shown to be involved in various biol. events, in addn. to the "housekeeping" phosphotransferase activity. We present the mol. cloning of a novel human NDP kinase gene, termed Nm23-H6. Nm23-H6 gene has been mapped at chromosome 3p21.3 and is highly expressed in heart, placenta, skeletal muscle, and some of the cancer cell lines. Recombinant Nm23-H6 protein has been identified to exhibit functional NDP kinase activity. Immunolocalization studies showed that both endogenous and inducibly expressed Nm23-H6 proteins were present as short, filament-like, perinuclear radical ***arrays*** and that they colocalized with ***mitochondria*** . Cell fractionation study also demonstrated the presence of Nm23-H6 protein in a mitochondria-rich fraction. Moreover, induction of overexpression of Nm23-H6 in SAOS2 cells, using the Cre-loxP gene activation system, resulted in growth suppression and generation of multinucleated cells. Flow cytometric anal. also demonstrated that the proportion of cells with more than 4N DNA content increased to 28.1% after induction of Nm23-H6, coinciding with the appearance of multinucleated cells. These observations suggest that Nm23-H6, a new member of the NDP kinase family, resides in mitochondria and plays a role in regulation of cell growth and cell cycle progression.
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 90 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:734521 CAPLUS <<LOGINID::20080906>>
DN 132:89117
TI Mitochondrial DNA repairs double-strand breaks in yeast chromosomes
AU Ricchetti, Miria; Fairhead, Cdcile; Dujon, Bernard
CS Unite de Physicochirnie des Macromolecules Biologiques (URA1773 du CNRS), Institut Pasteur, Paris, 75724, Fr.
SO Nature (London) (1999), 402(6757), 96-100 CODEN: NATUAS; ISSN: 0028-0836
PB Macmillan Magazines
DT Journal
LA English
AB The endosymbiotic theory for the origin of eukaryotic cells proposes that genetic information can be transferred from mitochondria to the nucleus of a cell, and genes that are probably of mitochondrial origin have been found in nuclear chromosomes. Occasionally, short or rearranged sequences homologous to mitochondrial DNA are seen in the chromosomes of different organisms including yeast, plants and humans. Here we report a mechanism by which fragments of ***mitochondrial*** DNA, in single or tandem ***array*** , are transferred to yeast chromosomes under natural conditions during the repair of double-strand breaks in haploid mitotic cells. These repair insertions originate from non- contiguous regions of the mitochondrial genome. Our anal. of the Saccharomyces cerevisiae mitochondrial genome indicates that the yeast nuclear genome does indeed contain several short sequences of mitochondrial origin which are similar in size and compn. to those that repair double-strand breaks. These sequences are located predominantly in non-coding regions of the chromosomes, frequently in the vicinity of retrotransposon long terminal repeats, and appear as recent integration events. Thus, colonization of the yeast genome by mitochondrial DNA is an ongoing process.
RE.CNT 30 THERE ARE 30 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 91 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:517860 CAPLUS <<LOGINID::20080906>>
DN 131:198920
TI Effects of vitamin E on the microstructural changes of renal tissue in streptozotocin-induced diabetic rats
AU Kwag, Oh-Gye; Im, Jung-Gyo; Rhee, Soon-Jae
CS Dept. of Nursing Science, Taegu Science College, Taegu, 702-722, S. Korea
SO Han'guk Sikp'um Yongyang Kwahak Hoechi (1999), 28(3), 663-669 CODEN: HSYHFB; ISSN: 1226-3311
PB Korean Society of Food Science and Nutrition
DT Journal
LA Korean
AB Male Sprague-Dawley rats weighing 100.+-.10 g were assigned to 1 normal (control) group and 3 groups with streptozotocin (STZ)-induced diabetes mellitus. The diabetic groups were fed vitamin E-free diet (DM-0E group), 40 mg vitamin E/kg diet (DM-40E group), and 400 mg vitamin E (as dl-.alpha.-tocopheryl acetate)/kg diet (DM-400E group). Dietary

vitamin E level in the normal group was 40 mg/kg feed. Diabetes was induced by i.v. injection of 55 mg STZ/kg body wt. in citrate buffer pH 4.3 after 4 wk on the diets. The animals were sacrificed 6 days later. The contents of thiobarbituric acid-reactive substances (TBARS) in kidneys were increased 119, 84, and 33% in the DM-0E, DM-40E, and DM-400E groups, resp., compared to controls. The level in the DM-400E group was decreased 39% compared to the DM-0E group. The content of .beta.2-microglobulin in urine in the DM-0E, DM-40E, and DM-400E groups were increased by 248, 181, and 164%, resp., compared to controls. The diabetic groups showed regressive lesions, such as intumescence and vacuolization of renal tubule epithelial cells. Electron microscopy of ***mitochondria*** in the proximal tubule epithelial cells showed irregular ***arrays*** , increase of ribosome content, and irregular arrangement of small villosity. These changes were more severe in the DM-0E group than in the DM-400E group. The TBARS prodn. in the kidney in the diabetic rats was increased, leading to damage of tubule fine structure. High intake of vitamin E suppressed the TBARS prodn. and improved the renal tissue peroxidative damage and relieved degenerative changes of renal tubule epithelial cells.

L26 ANSWER 92 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:218865 CAPLUS <<LOGINID::20080906>>
DN 131:41140
TI Mitochondrial telomere-binding protein from Candida parapsilosis suggests an evolutionary adaptation of a nonspecific single-stranded DNA-binding protein
AU Nosek, Jozef; Tomaska, L'ubomir; Pagacova, Blanka; Fukuhara, Hiroshi
CS Department of Biochemistry, Faculty of Natural Sciences, Comenius University, Bratislava, 842 15, Slovakia
SO Journal of Biological Chemistry (1999), 274(13), 8850-8857 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The mitochondrial genome in a no. of organisms is represented by linear DNA mols. with defined terminal structures. The telomeres of linear ***mitochondrial*** DNA (mtDNA) of yeast Candida parapsilosis consist of tandem ***arrays*** of large repetitive units possessing single-stranded 5' extension of about 110 nucleotides. Recently the authors identified the first mitochondrial telomere-binding protein (mtTBP) that specifically binds a sequence derived from the extreme end of C. parapsilosis linear mtDNA and protects it from attack by various DNA-modifying enzymes (Tomaska, L'., Nosek, J., and Fukuhara, H. (1997) J. Biol. Chem. 272, 3049-3059). Here the authors report the isolation of MTP1, the gene encoding mtTBP of C. parapsilosis. Sequence anal. revealed that mtTBP shares homol. with several bacterial and mitochondrial single-stranded DNA-binding proteins that nonspecifically bind to single-stranded DNA with high affinity. Recombinant mtTBP displays a preference for the telomeric 5' overhang of C. parapsilosis mtDNA. The heterologous expression of a mtTBP-GFP fusion protein resulted in its localization to the mitochondria but was unable to functionally substitute for the loss of the S. cerevisiae homolog Rim1p. Anal. of the MTP1 gene and its translation product mtTBP may provide an insight into the evolutionary origin of linear mitochondrial genomes and the role it plays in their replication and maintenance.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 93 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:149817 CAPLUS <<LOGINID::20080906>>
DN 130:349996
TI Mitochondrial DNA - structure, function and clinical relevance
AU Naumova, E.; Ivanova, M.; Ivanova, R.
CS Division of clinical and transplantation immunology, Medical University, Sofia, 1431, Bulg.
SO Balkan Journal of Medical Genetics (1998), 1(3), 91-94 CODEN: BJMGFN; ISSN: 1311-0160
PB DL&M Ltd.
DT Journal; General Review
LA English
AB A review with 39 refs. The human mitochondrial genome is very small and economically packed. The expression of the whole genome is essential for the maintenance of mitochondrial bioenergetic function. Mutations occur at a much higher rate in the mitochondrial DNA than in chromosomal DNA. These mutations appear to cause an extensive ***array*** of human degenerative disorders, known as ***mitochondrial*** diseases. The pathogenic role of cumulative mtDNA damage is being explored in many common diseases that develop late in life, and even in the aging process itself. Our knowledge of the mol. genetic basis of mitochondrial disease has already made it possible to develop sensitive and specific mol. tests for a no. of mitochondrial encephalomyopathies. The diagnosis of mitochondrial disorders by such methods is the first step in appropriate genetic treatment.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 94 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:51098 CAPLUS <<LOGINID::20080906>>
DN 130:206633
TI Search for novel redox groups in ***mitochondrial*** NADH:ubiquinone oxidoreductase (complex I) by diode ***array*** UV/VIS spectroscopy
AU Schulte, Ulrich; Abelmann, Anke; Amling, Natascha; Brors, Benedikt; Friedrich, Thorsten; Kintscher, Lars; Rasmussen, Tim; Weiss, Hanns
CS Institut fur Biochemie, Heinrich-Heine-Universitat Dusseldorf, Universitatsstrasse 1, Dusseldorf, D-40225, Germany
SO BioFactors (1998), 8(3,4), 177-186 CODEN: BIFAEU; ISSN: 0951-6433
PB IOS Press
DT Journal
LA English
AB The proton-translocating NADH:ubiquinone oxidoreductase of mitochondria (complex I) is a large L-shaped multisubunit complex. The peripheral matrix arm contains one FMN and a no. of iron-sulfur (FeS) clusters and is involved in NADH oxidn. and electron transfer to the membrane intrinsic arm. There, following a yet unknown mechanism, the redox-driven proton translocation and the ubiquinone redn. take place. Redox groups that would be able to link electron transfer with proton translocation have not been found so far in the membrane arm. We searched for such groups in complex I isolated from Neurospora crassa. Under anaerobic conditions, the prepn. was analyzed in different redox states by means of UV/VIS and EPR spectroscopy. Absorption bands in the UV/VIS redox difference spectra were found which cannot be attributed to the FMN or the EPR detectable FeS clusters. The existence of two novel groups is

postulated and their possible locations in the electron pathway and their roles in proton translocation are discussed.
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 95 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1999:2774 CAPLUS <<LOGINID::20080906>>
DN 130:165836
TI Flagellar mitochondrial association of the male-specific Don Juan protein in Drosophila spermatozoa
AU Santel, Ansgar; Blumer, Nicole; Kampfer, Matthias; Renkawitz-Pohl, Renate
CS Zoologie-Entwicklungsbiologie, Philipps-Universitat Marburg, Marburg, 35032, Germany
SO Journal of Cell Science (1998), 111(22), 3299-3309 CODEN: JNCSAI; ISSN: 0021-9533
PB Company of Biologists Ltd.
DT Journal
LA English
AB The Drosophila Don Juan gene encodes a basic protein (Don Juan protein), which is solely expressed postmeiotically during spermiogenesis in elongated spermatids and in mature sperm. Transgenic expression of a GFP-tagged Don Juan protein (DJ-GFP) in the male germ line showed an assocn. of the fusion protein with the sperm tail. Detailed examn. of DJ-GFP localization revealed novel insights into its distinct temporal and spatial distribution along the sperm tail during the last phase of spermatid maturation. Co-localization of DJ-GFP with actin-labeled cysts demonstrated its emergence in elongated spermatids during individualization. Addnl., the endogenous Don Juan protein was detected with epitope-specific antibodies in finally elongated nuclei of spermatids. After completion of nuclear shaping Don Juan is no longer detectable in the sperm heads with the onset of individualization. Mislocalization of the DJ-GFP protein in flagella of a mutant with defective mitochondrial differentiation provides evidence of ***mitochondrial*** assocn. of the fusion protein with flagellar ***mitochondrial*** ***arrays*** . Ectopically expressed DJ-GFP in premeiotic germ cells as well as salivary gland cells confirmed the capability of the fusion protein to assoc. with mitochondria. Therefore the authors suppose that Don Juan is a nuclear-encoded, germ-cell specifically expressed mitochondrial protein, which might be involved in the final steps of mitochondrial differentiation within the flagellum.
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 96 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1998:638351 CAPLUS <<LOGINID::20080906>>
DN 130:1881
TI Simultaneous analysis of the majority of low-molecular-weight, redox-active compounds from mitochondria
AU Kristal, Bruce S.; Vigneau-Callahan, Karen E.; Matson, Wayne R.
CS Dementia Research Service, Burke Medical Research Institute, White Plains, NY, 10605, USA
SO Analytical Biochemistry (1998), 263(1), 18-25 CODEN: ANBCA2; ISSN: 0003-2697
PB Academic Press
DT Journal
LA English
AB Studies of the interaction between oxidative stress and mitochondrial dysfunction are complicated by anal. limitations, esp. the need to assess multiple parameters in relatively small samples. We have addressed this problem by developing a methodol. for the simultaneous anal. of the majority of low-mol.-wt., redox-active compds. from ***mitochondria*** using HPLC sepns. followed by coulometric ***array*** detection. The method described should also be applicable for the study of redox-active compds. in other subcellular organelles as well as in intact cells and tissues. The protocol described enables simultaneous measurement of antioxidants (e.g., tocopherols, ascorbate, lipoates, uric and glutathione), markers of oxidative stress (e.g., o-tyrosine, m-tyrosine, nitrotyrosine, dityrosine, glutathione disulfide, and 8- hydroxydeoxyguanosine) as well as other metabolites (e.g., purines and indoles). In all, .apprx.600 redox active compds. can be detected, most with a limit of detection of .apprx.5 pg on column. Results, including anal. parameters, from a study of liver mitochondria from control and diabetic rats are presented to demonstrate utility of this methodol. (c) 1998 Academic Press.
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 97 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1998:110816 CAPLUS <<LOGINID::20080906>>
DN 128:229011
OREF 128:45345a,45348a
TI Mitochondrial DNA and diseases of the nervous system: the spectrum
AU Dimauro, Salvatore; Schon, Eric A.
CS H. Houston Merritt Clinical Research Center for Muscular Dystrophy and Related Diseases, Departments of Neurology and Genetics and Development, Columbia University College of Physicians and Surgeons, New York, NY, 10032, USA
SO Neuroscientist (1998), 4(1), 53-63 CODEN: NROSFJ; ISSN: 1073-8584
PB Williams & Wilkins
DT Journal; General Review
LA English
AB A review with 60 refs. The past 9 yr have witnessed the development of a new chapter in human pathol. related to mutations in the "other genome" or the "25th chromosome," namely mitochondrial DNA (mtDNA). An astounding ***array*** of multisystemic disorders, almost always involving muscle and brain (***mitochondrial*** encephalomyopathies) have been attributed to over 50 point mutations and a multitude of rearrangements in mtDNA. Here, the authors review the still expanding spectrum of proven or putative mtDNA-related disorders, and the authors try to explain some peculiarities of these diseases according to the new rules of "mitochondrial genetics.".
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 98 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:784828 CAPLUS <<LOGINID::20080906>>
DN 128:124333
OREF 128:24271a,24274a
TI Evolutionary dynamics of tandem repeats in the mitochondrial DNA control region of the minnow Cyprinella spiloptera
AU Broughton, Richard E.; Dowling, Thomas E.

CS Department of Zoology, Arizona State University, AZ, USA
SO Molecular Biology and Evolution (1997), 14(12), 1187-1196 CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB Length variation due to tandem repeats is now recognized as a common feature of animal mitochondrial DNA; however, the evolutionary dynamics of repeated sequences are not well understood. Using phylogenetic anal., predictions of three models of repeat evolution were tested for arrays of 260-bp repeats in the cyprinid fish Cyprinella spiloptera. Variation at different nucleotide positions in individual repeats supported different models of repeat evolution. One set of characters included several nucleotide variants found in all copies from a limited no. of individuals, while the other set included an 8-bp deletion found in a limited no. of copies in all individuals. The deletion and an assocd. nucleotide change appear to be the result of a deterministic, rather than stochastic, mutation process. Parallel origins of repeat ***arrays*** in different ***mitochondrial*** lineages, possibly coupled with a homogenization mechanism, best explain the distribution of nucleotide variation.
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 99 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:778851 CAPLUS <<LOGINID::20080906>>
DN 128:74676
OREF 128:14599a
TI Histopathologic and ultrastructural alterations of white liver disease in sheep experimentally depleted of cobalt
AU Kennedy, S.; Mcconnell, S.; Anderson, H.; Kennedy, D. G.; Young, P. B.; Blanchflower, W. J.
CS Veterinary Sciences Division, Department of Agriculture for Northern Ireland, Belfast, UK
SO Veterinary Pathology (1997), 34(6), 575-584 CODEN: VTPHAK; ISSN: 0300-9858
PB American College of Veterinary Pathologists
DT Journal
LA English
AB Many cobalt-deficient sheep develop liver lesions known as ovine "white liver" disease, but the etiol. of these changes is controversial. It has been suggested that cofactors are required for development of liver damage in cobalt-deficient sheep. In this study, one group of lambs (n=5) was fed a diet low in cobalt (4.5 .mu.g/kg) while a group of control lambs (n=4) received the same diet after it had been supplemented with cobalt (1000 .mu.g/kg). All cobalt-depleted lambs had reduced growth rate, anorexia, lacrimation, and alopecia, and they eventually became emaciated (mean body wt. at end of study: 83% of initial body wt.). Plasma concns. of bilirubin and serum activity of glutamate-oxaloacetate transferase were elevated in these animals, while plasma concns. of vitamin B12 were reduced (less than 220 pmol/L from day 42). Fatty degeneration of the liver assocd. with reduced concns. of vitamin B12 (14.5 pmol/g) was seen in these animals at necropsy at 196 days. Microscopic liver lesions included accumulation of lipid droplets and lipofuscin particles in hepatocytes, dissocn. and necrosis of hepatocytes, and sparse infiltration by neutrophils, macrophages, and lymphocytes. Ultrastructural hepatocytic alterations included swelling, condensation and proliferation of ***mitochondria*** , hypertrophy of smooth endoplasmic reticulum, vesiculation and loss of ***arrays*** of rough endoplasmic reticulum, and accumulation of lipid droplets and lipofuscin granules in cytoplasm of hepatocytes. No liver lesions were seen in control lambs. The results of this study indicate that cofactors are not a prerequisite to development of hepatic damage in cobalt-deficient sheep. Reduced activities of the vitamin B12-dependent enzymes, methylmalonyl CoA mutase and methionine synthase, and lipid peroxidn. are of likely pathogenetic importance in the development of the lesions.
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 100 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:642877 CAPLUS <<LOGINID::20080906>>
DN 127:303928
OREF 127:59310h,59311a
TI Evolution of repeated sequence ***arrays*** in the D-loop region of bat ***mitochondrial*** DNA
AU Wilkinson, Gerald S.; Mayer, Frieder; Kerth, Gerald; Petri, Barbara
CS Department of Zoology, University of Maryland, College Park, MD, 20742, USA
SO Genetics (1997), 146(3), 1035-1048 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB Anal. of mitochondrial DNA control region sequences from 41 species of bats representing 11 families revealed that repeated sequence arrays near the tRNA-Pro gene are present in all vespertilionine bats. Across 18 species tandem repeats varied in size from 78 to 85 bp and contained two to nine repeats. Heteroplasmy ranged from 15% to 63%. Fewer repeats among heteroplasmic than homoplasmic individuals in a species with up to nine repeats indicates selection may act against long arrays. A lower limit of two repeats and more repeats among heteroplasmic than homoplasmic individuals in two species with few repeats suggests length mutations are biased. Significant regressions of heteroplasmy, .theta. and .pi., on repeat no. further suggest that repeat duplication rate increases with repeat no. Comparison of vespertilionine bat consensus repeats to mammal control region sequences revealed that tandem repeats of similar size, sequence and no. also occur in shrews, cats and bighorn sheep. The presence of two conserved protein-binding sequences in all repeat units indicates that convergent evolution has occurred by duplication of functional units. It is speculated that D-loop region tandem repeats may provide signal redundancy and a primitive repair mechanism in the event of somatic mutations to these binding sites.
RE.CNT 75 THERE ARE 75 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 101 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:634342 CAPLUS <<LOGINID::20080906>>
DN 127:290871
OREF 127:56777a,56780a
TI Genetic structure of the flounders Platichthys flesus and P. stellatus at different geographic scales
AU Borsa, P.; Blanquer, A.; Berrebi, P.
CS Lab. Genome Populations, UPR CNRS, Univ. Montpellier, Montpellier, F-34095, Fr.
SO Marine Biology (Berlin) (1997), 129(2), 233-246 CODEN: MBIOAJ; ISSN: 0025-3162

PB Springer
DT Journal
LA English
AB The genetic structure of the flounders Platichthys flesus L. and P. stellatus Pallas was investigated on different spatial scales through anal. of allozyme variation at 7 to 24 polymorphic loci in samples collected from different regions (Baltic Sea, North Sea, Brittany, Portugal, western Mediterranean, Adriatic Sea, Aegean Sea and Japan) in 1984 to 1987. No geog. variation was evident within a region. Some pattern of differentiation by distance was inferred within the Atlantic, while the Mediterranean comprised three geog. isolated populations and was itself geog. from the Atlantic (fixed allele differences at up to three loci were found among P. flesus populations from the Atlantic, the western Mediterranean, the Adriatic Sea, the Aegean Sa and also P. stellatus from the coast of Japan). Sea temp. during the reproductive period probably acts as a barrier to gene flow between populations. Genetic distances among European flounder populations (P. flesus) were higher than, or of the same magnitude as, the genetic distance between Pacific (P. stellatus) and European flounder populations, suggesting that P. flesus is paraphyletic and/or there is no phylogenetic basis to recognizing P. stellatus as a different species. The divergence between P. flesus and P. stellatus was thus inferred to be more recent than the divergence between the present P. flesus populations from the NE Atlantic and eastern Mediterranean. The eastern Mediterranean populations are thought to originate from the colonization of the Mediterranean by a proto-P. flesus/P. stellatus ancestor, whereas the present western Mediterranean population has undergone a more recent colonization event by P. flesus. Patterns of ***mitochondrial*** DNA variation, established on a smaller ***array*** of P. flesus samples, were in accordance with the geog. patterns inferred from the allozyme survey. In addn., they supported the hypothesis of a two-step colonization of the western Mediterranean. These results contribute to our understanding of the biogeog. of the Mediterranean marine fauna, esp. the group of boreal remnants to which P. flesus belongs.
RE.CNT 79 THERE ARE 79 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 102 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1997:503029 CAPLUS <<LOGINID::20080906>>
DN 127:200844
OREF 127:38875a,38878a
TI Nonneutral evolution of tandem repeats in the mitochondrial DNA control region of lagomorphs
AU Casane, D.; Dennebouy, N.; de Rochambeau, H.; Mounolou, J. C.; Monnerot, M.
CS Cent. Genetique Mol. CNRS, Fr.
SO Molecular Biology and Evolution (1997), 14(8), 779-789
CODEN: MBEVEO; ISSN: 0737-4038
PB Society for Molecular Biology and Evolution
DT Journal
LA English
AB The ***mitochondrial*** DNA of the European rabbit (Oryctolagus cuniculus) contains a tandem ***array*** of 153-bp repeats in the vicinity of the replication origin of the H-strand. Variation among mols. in the no. of these repeats results in inter- and intraindividual length polymorphism (heteroplasmy). Generally, in an individual, one predominant mol. type is obsd., the others representing a low percentage of the mtDNA content. At the tissue level, we observe a particular distribution of this polymorphism in the gonads compared with liver, kidneys, or brain, implying a relationship between the differentiation status of the cells and the types of new mtDNA mols. which appear and accumulate during lifetime. Similar tandem repeats were also found in the mtDNA noncoding region of European hares (Lepus europaeus), a cottontail (Sylvilagus floridanus), and a pika (Ochotona refuscens). The lengths and the sequences of these units evolve rapidly and in a concerted way, but the no. of repeats is maintained in a narrow range, and an internal 20-bp segment is highly conserved. Constraints restrict the evolution of the primary sequence of these repeated units, the no. of which is probably controlled by a stabilizing selection.

L26 ANSWER 103 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:641840 CAPLUS <<LOGINID::20080906>>
DN 125:294156
OREF 125:54827a,54830a
TI Accessing genetic information with high-density DNA arrays
AU Chee, Mark; Yang, Robert; Hubbell, Earl; Berno, Anthony; Huang, Xiaohua C.; Stern, David; Winkler, Jim; Lockhart, David J.; Morris, Macdonald S.; Fodor, Stephen P. A.
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Science (Washington, D. C.) (1996), 274(5287), 610-614
CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
AB Rapid access to genetic information is central to the revolution taking place in mol. genetics. The simultaneous anal. of the entire human mitochondrial genome is described here. DNA arrays contg. up to 135,000 probes complementary to the 16.6-kilobase human mitochondrial genome were generated by light-directed chem. synthesis. A two-color labeling scheme was developed that allows simultaneous comparison of a polymorphic target to a ref. DNA or RNA. Complete hybridization patterns were revealed in a matter of minutes. Sequence polymorphisms were detected with single-base resoln. and unprecedented efficiency. The methods described are generic and can be used to address a variety of questions in mol. genetics including gene expression, genetic linkage, and genetic variability.

L26 ANSWER 104 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:305225 CAPLUS <<LOGINID::20080906>>
DN 125:2389
OREF 125:559a,562a
TI DNA sequencing using four-color capillary array electrophoresis and energy transfer primers
AU Kheterpal, Indu; Ju, Jingyue; Radhakrishnan, Arun; Brandt, Gabriel S.; Ginther, Charles L.; Clark, Steven M.; Scherer, James R.; Sensabaugh, George F.; Mathies, Richard A.
CS Department of Chemistry, University of California, Berkeley, CA, USA
SO Proceedings of SPIE-The International Society for Optical Engineering (1996), 2680(Ultrasensitive Biochemical Diagnostics), 204-213 CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
AB A practical capillary array electrophoresis sequencer has been constructed and tested for large scale DNA sequencing. This system employs a scanning confocal optical system to detect DNA fragments electrophoresed on a capillary array. By using the recently developed energy transfer fluorescent primers, sensitive four-color detection is facilitated while exciting with just a single laser wavelength (488 nm) from an argon ion laser.

Software for facile redn. of the images to four-color trace files and for automated base-calling have also been developed. This system can detect up to 25 capillaries at a time and has a raw sequencing rate of .apprx. 6 kilobases/h. Applications to mitochondrial D-loop DNA sequencing are presented as a demonstration.

L26 ANSWER 105 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:120103 CAPLUS <<LOGINID::20080906>>
DN 124:195486
OREF 124:35955a,35958a
TI Recombination between heterologous linear and circular mitochondrial plasmids in the fungus Neurospora
AU Griffiths, Anthony J. F.; Yang, Xiao
CS Botany Dep., Univ. British Columbia, Vancouver, BC, V6T 1Z4, Can.
SO Molecular & General Genetics (1995), 249(1), 25-36 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer
DT Journal
LA English
AB A strain of Neurospora intermedia from China contains five prominent extragenomic mitochondrial plasmids: three linear elements called zhisi plasmids, and two circular plasmids, Harbin-1 and -2. In one subculture, levels of four plasmids (all three zhisis and Harbin-1) fell to undetectable values and two novel linear plasmids appeared, Harbin-L and L-2, as well as a new small circular plasmid, Harbin-0.9. Cross-hybridization of restriction fragments and DNA sequencing showed that the Harbin-L plasmid was composed of parts of the circular Harbin-1 plasmid and of one of the linear zhisi plasmids. A model is presented in which the Harbin-1 and zhisi plasmids are present within the same mitochondrion, and crossovers at two sep. 7 bp sites of sequence identity effectively insert part of the circular Harbin-1 DNA into a zhisi element. The small plasmid Harbin-0.9 is a fragment of the Har-1 plasmid, and seems to be another product of the recombination process that created Har-L. Recombination of this type could have contributed to the wide ***array*** of ***mitochondrial*** plasmids found in natural populations of Neurospora.

L26 ANSWER 106 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:52282 CAPLUS <<LOGINID::20080906>>
DN 124:107767
OREF 124:19923a,19926a
TI 17. Mitochondrial DNA in somatic hybrids and cybrids
AU Earle, Elizabeth D.
CS Dep. Plant Breeding, Biometry, Cornell Univ., Ithaca, NY, USA
SO Advances in Cellular and Molecular Biology of Plants (1995), 3(Molecular Biology of Plant Mitochondria), 557-84 CODEN: ACMBEF; ISSN: 1381-1932
PB Kluwer
DT Journal; General Review
LA English
AB A review with 112 refs. Protoplast fusion provides an efficient method for producing plants with new combinations of nuclei, chloroplasts, and mitochondria. Mitochondrial DNA in somatic hybrids or cybrids often contains regions contributed by both fusion partners as well as novel fragments that probably represent intergenomic recombination. Many studies in this area are descriptive; they simply classify the mitochondrial DNA as similar to one of the other fusion partners or as non-parental on the basis of stained gels of mitochondrial DNA restriction digests of hybridization of a limited no. of probes to total DNA. Distribution of mitochondrial DNA regions from the fusion partners in the fusion products is often not random, but there is as yet no consistent exptl. method to achieve a particular desired outcome. Taxonomic relationships between the source of the nucleus and mitochondria can influence the results seen, and there are also "hot spots" for recombination. Fusion products with an ***array*** of ***mitochondrial*** DNA rearrangements make it possible to correlate ***mitochondrially*** encoded phenotypes such as cytoplasmic male sterility with specific regions of mitochondrial DNA. Fusion manipulations involving mitochondria also provide several promising ways to create new and possibly useful plant types.

L26 ANSWER 107 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1996:28763 CAPLUS <<LOGINID::20080906>>
DN 124:82553
OREF 124:15393a,15396a
TI Oxygen and pH regulation of protein synthesis in mitochondria from Artemia franciscana embryos
AU Kwast, Kurt E.; Hand, Steven C.
CS Department Environmental Population Organismic Biology, University Colorado, Boulder, CO, 80309-0334, USA
SO Biochemical Journal (1996), 313(1), 207-13 CODEN: BIJOAK; ISSN: 0264-6021
PB Portland Press
DT Journal
LA English
AB To identify factors responsible for the down-regulation of mitochondrial biosynthetic processes during anoxia in encysted Artemia franciscana embryos, the effects of oxygen limitation and pH on protein synthesis were investigated in isolated mitochondria. At the optimal pH of 7.5, exposure of mitochondria to anoxia decreases the protein synthesis rate by 79%. Rates were suppressed by a further 10% at pH 6.8, the intracellular pH (pHi) measured under anoxia in vivo. Matrix pH, measured under identical conditions, was 8.43 at an extramitochondrial pH of 7.9, 8.05 at pH 7.5, and 7.10 at pH 6.8. The matrix pH did not vary as a function of oxygen availability during the 1 h assays. Intramitochondrial purine nucleotides varied little as a function of pH. In contrast, after 1 h of protein synthesis under anoxia, ATP levels decreased by up to 40%, whereas AMP, ADP and GDP concns. increased, and GTP and GMP concns. remained relatively const. The addn. of 1 mM ATP at the onset of anoxia maintained the ATP/ADP ratio at the aerobic value, but did not stabilize the GTP/GDP ratio or rescue rates of protein synthesis. Thus, at present, the authors cannot eliminate the possibility that the decrease in the GTP/GDP ratio during anoxia may contribute to the suppression of protein synthesis. The effect of anoxia was reversible; the rate of protein synthesis upon reoxygenation after a 30 min bout of anoxia was comparable with the pre-anoxic rate (193 and 174 pmol of leucine per mg of protein, resp.). The ***array*** of ***mitochondrial*** translation products did not differ qual. as a function of either oxygen availability or pH. Finally, similar pH profiles for protein synthesis were obtained with either [3H]leucine or [3H]histidine (known to use different transporters). Consequently, it is improbable that the pH-sensitivity of protein synthesis can be explained by a specific protein effect on the import of the radiolabeled amino acid used. In summary, both oxygen limitation and acidic pH suppress rates of mitochondrial protein synthesis and are likely to contribute to the arrest of mitochondrial anabolic processes during anoxia-induced quiescence in A. franciscana embryos.

L26 ANSWER 108 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1995:950270 CAPLUS <<LOGINID::20080906>>
DN 124:79759
OREF 124:14793a,14796a
TI Characterization of S-AKAP84, a novel developmentally regulated a kinase anchor protein of male germ cells
AU Lin, Reigh-Yi; Moss, Stuart B.; Rubin, Charles S.
CS Atran Lab., Albert Einstein Coll. Med., Bronx, NY, 10461, USA
SO Journal of Biological Chemistry (1995), 270(46), 27804-11 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Bio logy
DT Journal
LA English
AB In mammalian spermatozoa, most of the type II.alpha. isoform of cAMP-dependent protein kinase (PKAII.alpha.) is anchored at the cytoplasmic surface of a specialized ***array*** of ***mitochondria*** in the flagellar cytoskeleton. This places the catalytic subunits of PKAII.alpha. in proximity with potential target substrates in the cytoskeleton. The mechanism by which PKAII.alpha. is anchored at the outer surface of germ cell mitochondria has not been elucidated. We now report the cloning of a cDNA that encodes a novel, germ cell A kinase anchor protein (AKAP) designated S-AKAP84. S-AKAP84 comprises 593 amino acids and contains a centrally located domain that avidly binds regulatory subunits (RII.alpha. and RII.beta.) of PKAII.alpha. and PKAII.beta.. Te 3.2-kilobase S-AKAP84 mRNA and the principally in the male germ cell lineage. Expression of S-KAP84 is tightly regulated during development. The protein accumulates as spermatids undergo nuclear condensation and tail elongation. The timing of S-AKAP84 expression is correlated with the de novo accumulation of RII.alpha. and RII.beta. subunits and the migration of mitochondria from the cytoplasm (round spermatids) to the cytoskeleton (midpiece in elongating spermatids). Residues 1-30 at the NH2 terminus of S-AKAP84 constitute a putative signal/anchor sequence that may target the protein to the outer mitochondrial membrane. Immunofluorescence anal. demonstrated that S-AKAP84 is co-localized with mitochondria in the flagellum.

L26 ANSWER 109 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1995:685112 CAPLUS <<LOGINID::20080906>>
DN 123:79313
OREF 123:14035a,14038a
TI Actin-dependent mitochondrial motility in mitotic yeast and cell-free systems: identification of A motor activity on the mitochondrial surface
AU Simon, Viviana R.; Swayne, Theresa C.; Pon, Liza A.
CS Dep. of Anatomy and Cell Biology, Columbia Univ., New York, NY, 10032, USA
SO Journal of Cell Biology (1995), 130(2), 345-54 CODEN: JCLBA3; ISSN: 0021-9525
PB Rockefeller University Press
DT Journal
LA English
AB Using fluorescent membrane potential sensing dyes to stain budding yeast, ***mitochondria*** are resolved as tubular organelles aligned in radial ***arrays*** that coverage at the bud neck. Time-lapse fluorescence microscopy reveals region-specific, directed mitochondrial movement during polarized yeast cell growth and mitotic cell division. Mitochondria in the central region of the mother cell move linearly towards the bud, traverse the bud neck, and progress towards the bud tip at an av. velocity of 49 .+-. 21 nm/s. In contrast, mitochondria in the peripheral region of the mother cell and at the bud tip display significantly less movement. Yeast strains contg. temp. sensitive lethal mutations in the actin gene show abnormal mitochondrial distribution. No mitochondrial movement is evident in these mutants after short-term shift to semipermissive temps. Thus, the actin cytoskeleton is important for normal mitochondrial movement during inheritance. To det. the possible role of known myosin genes in yeast mitochondrial motility, we investigated mitochondrial inheritance in myo1, myo2, myo3 and myo4 single mutants and in a myo2, myo4 double mutant. Mitochondrial spatial arrangement and motility are not significantly affected by these mutations. We used a microfilament sliding assay to examine motor activity on isolated yeast mitochondria, as well as unilamellar, right-side-out, sealed mitochondrial outer membrane vesicles. In the presence of low levels of ATP (0.1-100 .mu.M), we observe F-actin sliding on immobilized yeast mitochondria. In the presence of high levels of ATP (500 .mu.M-2 mM), bound filaments are released from mitochondria and mitochondrial outer membranes. The max. velocity of mitochondria-driven microfilament sliding (23 .+-. 11 nm/s) is similar to that of mitochondrial movement in living cells. This motor activity requires hydrolysis of ATP, does not require cytosolic exts., is sensitive to protease treatment, and displays an ATP concn. dependence similar to that of members of the myosin family of actin-based motors. This is the first demonstration of an actin-based motor activity in a defined organelle population.

L26 ANSWER 110 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1994:595026 CAPLUS <<LOGINID::20080906>>
DN 121:195026
OREF 121:35127a,35130a
TI Schwann cell mitochondrial alterations in peripheral nerves of rabbits treated with 2',3'-dideoxycytidine
AU Feldman, Dorothy; Anderson, Timothy D.
CS Department Investigative Toxicology, Hoffmann-La Roche Inc., Nutley, NJ, 07110, USA
SO Acta Neuropathologica (1994), 87(1), 71-80 CODEN: ANPTAL; ISSN: 0001-6322
DT Journal
LA English
AB 2',3'-Dideoxycytidine (ddC) is a nucleoside analog and reverse-transcriptase inhibitor that is approved for treatment of AIDS patients. A rabbit model of ddC neurotoxicity was developed to help understand the dose-limiting clin. neurotoxicity of ddC. Rabbits with a myelinopathy resulting from treatment with ddC exhibited mitochondrial alterations in Schwann cells of sciatic and tibial nerves and dorsal root ganglia. These changes were initially evident after 16 wk of oral treatment with 35 mg/kg per day of ddC and were pos. correlated with myelin pathol. in individual animals. Cup-shaped ***mitochondria*** were frequently obsd.; when these ***mitochondria*** occurred in multiple concentric ***arrays*** or at various angles to one another, different profiles were formed depending on the plane of section. An increased no. of mitochondrial cristae assumed a tubular configuration. It is suggested that the complex aggregations of mitochondria seen in this expt. are an adaptive response to altered mitochondrial function caused by treatment with ddC.

L26 ANSWER 111 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1994:526691 CAPLUS <<LOGINID::20080906>>
DN 121:126691
OREF 121:22709a,22712a

TI Rapid evolution of a heteroplasmic repetitive sequence in the mitochondrial DNA control region of carnivores
AU Hoelzel, A. Rus; Lopez, Jose V.; Dover, Gabriel A.; O'Brien, Stephen J.
CS Lab. Viral Carcinogenesis, National Cancer Inst., Frederick, MD, 21702, USA
SO Journal of Molecular Evolution (1994), 39(2), 191-9 CODEN: JMEVAU; ISSN: 0022-2844
DT Journal
LA English
AB The authors described a repetitive DNA region at the 3' end of the mitochondrial DNA (mtDNA) control region and compare it in 21 carnivore species representing eight carnivore families. The sequence and organization of the repetitive motifs can differ extensively between arrays; however, all motifs appear to be derived from the core motif "ACGT". Sequence data and Southern blot anal. demonstrate extent heteroplasmy. The general form of the array is similar between heteroplasmic variants within an individual and between individuals within a species (varying primarily in the length of the array, though two clones form the northern elephant seal are exceptional). Within certain families, notably ursids, the array structure is also similar between species. Similarly between species was not apparent in other carnivore families, such as the mustelids, suggesting rapid changes in the organization and sequence of some arrays. The pattern of change seen within and between species suggests that a dominant mechanism involved in the evolution of these arrays is DNA slippage. A comparative anal. shows that the motifs that are being reiterated or deleted vary within and between arrays, suggesting a varying rate of DNA turnover. The authors discuss the evolutionary implications of the obsd. patterns of variation and extreme levels of heteroplasmy.

L26 ANSWER 112 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1994:212325 CAPLUS <<LOGINID::20080906>>
DN 120:212325
OREF 120:37529a,37532a
TI Microtubules regulate the generation of polarity in zoospores of Phytophthora cinnamomi
AU Hyde, Geoffrey J.; Hardham, Adrienne R.
CS Res. Sch. Biol. Sci., Aust. Natl. Univ., Canberra, Australia
SO European Journal of Cell Biology (1993), 62(1), 75-85 CODEN: EJCBDN; ISSN: 0171-9335
DT Journal
LA English
AB Zoospores of Phytophthora cinnamomi are formed by cleavage of a multinucleate sporangium and contain nine different components that are distributed or oriented about a well-defined axis running through a pair of basal bodies near the nucleus. In this study, the importance of the cytoskeleton in establishing and maintaining cellular polarity was examd. by using the anti-microtubule drug oryzalin and the anti-microfilament drug cytochalasin D (CD). The effects of the drugs on uncleaved and cleaving sporangia were detd., using fluorescence microscopy, for six of the components that are polarized in untreated cleaved cells: an astral microtubule (MT) ***array*** , the nucleus, ***mitochondria*** and three different types of vesicles, two of which are involved in directed exocytosis. CD had no effect upon the MT ***arrays*** , the positioning of nuclei or the polarized redistribution of ***mitochondria*** and vesicles to the cortical cytoplasm, although it did cause abnormal cleavage. The effects of oryzalin, however, indicate that the asym. disposition of the MT array is fundamental to zoospore polarities: when the array is itself eliminated with this drug, none of the other five elements show any signs of polar positioning within the cleaved sporangium. Oryzalin also caused abnormal cleavage similar to that seen in CD-treated cells. Most intriguing, however, was the finding that although the three vesicle types in cleaved, oryzalin-treated sporangia did not exhibit the polarized distribution seen in control and CD-treated cells, in many cases the vesicles had, nevertheless, lost their initially random distributions and had become concd. in the cytoplasm adjacent to the abnormal cleavage planes. Thus although an intact MT array is required for segregation of the vesicles within the cortex, their redistribution to the cortex can somehow occur in the absence of MTs and actin microfilaments.

L26 ANSWER 113 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1994:49909 CAPLUS <<LOGINID::20080906>>
DN 120:49909
OREF 120:9047a,9050a
TI Unidirectional dominance of cytoplasmic inheritance in two genetic crosses of Plasmodium falciparum
AU Vaidya, Akhil B.; Morrisey, Joanne; Plowe, Christopher V.; Kaslow, David C.; Wellems, Thomas E.
CS Hahnemann Univ., Philadelphia, PA, 20892, USA
SO Molecular and Cellular Biology (1993), 13(12), 7349-57 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB Malarial parasites have 2 highly conserved cytoplasmic DNA mols.: a 6-kb tandemly ***arrayed*** DNA that has characteristics of a ***mitochondrial*** genome, and a 35-kb circular DNA that encodes functions commonly found in chloroplasts. The authors examd. the inheritance pattern of these elements in 2 genetic crosses of Plasmodium falciparum clones. Parent-specific oligonucleotide probes and single-strand conformation polymorphism anal. identified single nucleotide changes that distinguished the parental 6- and 35-kb DNA mols. in the progeny. In all 16 independent recombinant progeny of a cross between a Central American clone, HB3, and a Southeast Asian clone, Dd2, the 6- and 35-kb DNAs were inherited from the Dd2 parent. In all 9 independent recombinant progeny of a cross between clone HB3 and a likely African clone, 3D7, the 6-kb DNA was inherited from the 3D7 parent. Inheritance of cytoplasmic genomes of the Dd2 and 3D7 parents was, therefore, dominant over that of the HB3 parent. Cytoplasmic DNA mols. were found almost exclusively in the female gametes of malarial parasites; hence, clone HB3 did not appear to have served as a maternal parent for the progeny of 2 crosses. Defective differentiation into male gametes by clone Dd2 is likely to be a reason for the cytoplasmic inheritance pattern seen in the HB3 .times. Dd2 cross. However, incompetence of male or female games is unlikely to explain the uniparental dominance in recombinant progeny of the HB3 .times. 3D7 cross, since both parents readily self-fertilized and completed the malaria life cycle on their own. Instead, the data suggest unidirectional parental incompatibility in cross-fertilization of these malarial parasites, where a usually cosexual parental clone can participate only as a male or as a female. Such an incompatibility may be speculated as indicating an early phase of reproductive isolation of P. falciparum clones from different geog. regions.

L26 ANSWER 114 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1993:206554 CAPLUS <<LOGINID::20080906>>
DN 118:206554
OREF 118:35364h,35365a

TI Heteroplasmy of short tandem repeats in mitochondrial DNA of Atlantic cod, Gadus morhua
AU Arnason, Einar; Rand, David M.
CS Mus. Comp. Zool., Harvard Univ., Cambridge, MA, 02138, USA
SO Genetics (1992), 132(1), 211-20 CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB The ***mitochondrial*** DNA of the Atlantic cod (G. morhua) contains a tandem ***array*** of 40-bp repeats in the D-loop region of the mol. Variation among mols. in the copy no. of these repeats results in mtDNA length variation and heteroplasmy (the presence of more than one form of mtDNA in an individual). In a sample of fish collected from different localities around Iceland and off George's Bank, each individual was heteroplasmic for 2 or more mtDNAs ranging in repeat copy no. from 2 (common) to 6 (rare). An earlier report on mtDNA heteroplasmy in sturgeon (Acipenser transmontanus) presented a competitive displacement model for length mutations in mtDNAs contg. tandem arrays and the cod data deviate from this model. Depending on the nature of putative secondary structures and the location of D-loop strand termination, addnl. mechanisms of length mutation may be needed to explain the range of mtDNA length variants maintained in these populations. The balance between genetic drift and mutation in maintaining this length polymorphism is estd. through a hierarchical anal. of diversity of mtDNA length variation in the Iceland samples. Eighty percent of the diversity lies within individuals, 8% among individuals and 12% among localities. An est. of .theta. = 2Neo.mu. > 1 indicates that this system is characterized by a high mutation rate and is governed primarily by deterministic dynamics. The sequences of repeat arrays from fish collected in Norway, Iceland and George's Bank show no nucleotide variation suggesting that there is very little substructuring to the North Atlantic cod population.

L26 ANSWER 115 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1992:607401 CAPLUS <<LOGINID::20080906>>
DN 117:207401
OREF 117:35677a,35680a
TI Classification of projection images of crystalline ***arrays*** of the ***mitochondrial*** , voltage-dependent anion-selective channel embedded in aurothioglucose
AU Guo, Xiao Wei; Mannella, Carmen A.
CS Wadsworth Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201-0509, USA
SO Biophysical Journal (1992), 63(2), 418-27 CODEN: BIOJAU; ISSN: 0006-3495
DT Journal
LA English
AB Low-dose electron microscopic images have been recorded from membrane crystals of the mitochondrial voltage-dependent anion-selective channel, embedded in aurothioglucose. There is considerable variation in the high-resoln. detail present in correlation avs. computed from these images. Correspondence anal. reveals three classes of control avs., with main components of variation involving projected size of the pores and d. modulations around the pores and in the corners of the unit cells away from the pores. Pretreatments that affect the functional state of the channel also affect the array avs. In particular, there appears to be a general correlation between the expected effector-induced state (i.e., open and closed) and the projected diam. of the channel lumens in the cryst. arrays.

L26 ANSWER 116 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1992:506789 CAPLUS <<LOGINID::20080906>>
DN 117:106789
OREF 117:18497a,18500a
TI Structure of paracrystalline ***arrays*** on outer membranes of rat-liver and rat-heart ***mitochondria***
AU Mannella, C. A.; Ribeiro, A.; Cognon, B.; D'Arcangelis, D.
CS Wadsworth Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201-0509, USA
SO Journal of Structural Biology (1992), 108(3), 227-37 CODEN: JSBIEM; ISSN: 1047-8477
DT Journal
LA English
AB Cryst. arrays are induced in outer membranes of rat-liver and rat-heart mitochondria by phosphotungstate and silicotungstate. The basic structure of the arrays has been detd. by correlation averaging of electron microscopic images of side views of tubular arrays and en face views of planar arrays. The arrays consist of rows of bilobed projecting subunits and are similar (in lattice parameters and projected subunit dimensions) to periodic arrays of ion transport ATPases, e.g., arrays of Ca2+-ATPase induced by vanadate in sarcoplasmic reticulum. Hexokinase-labeled colloidal gold particles do not specifically decorate the arrays, suggesting that the hexokinase receptor (VDAC channel) is not a component of the arrays.

L26 ANSWER 117 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1991:98762 CAPLUS <<LOGINID::20080906>>
DN 114:98762
OREF 114:16782h,16783a
TI High-resolution localization of hyaluronic acid in the golden hamster oocyte-cumulus complex by use of a hyaluronidase-gold complex
AU Kan, Frederick W. K.
CS Fac. Med., Univ. Montreal, Montreal, QC, H3C 3J7, Can.
SO Anatomical Record (1990), 228(4), 370-82 CODEN: ANREAK; ISSN: 0003-276X
DT Journal
LA English
AB The distribution of hyaluronic acid in the oocyte-cumulus complexes collected from the oviduct ampulla of superovulated hamsters was revealed by use of hyaluronidase coupled to colloidal Au. On thin sections of Lowicryl-embedded oocyte-cumulus complexes, Au particles were assocd. specifically with interconnecting fibrillar materials that make up the cumulus matrix. Inside the cumulus cells, Au particles were found over the cisternal membrane of the rough endoplasmic reticulum, in the contents of lysosomes and multivesicular bodies, and over Golgi vesicles of some cumulus cells. A high concn. of Au labeling was obsd. over the peripheral condensed chromatin and perinucleolar components in the nucleus. The cell surface of the cumulus cells also appeared to be labeled. Au particles, however, were absent over the mitochondria and lipid vacuoles. In the oocytes, labeling was found to be assocd. mainly with rough endoplasmic reticulum and ***arrays*** of lamellar structures; cortical granules, ***mitochondria*** , and coated vesicles were essentially devoid of Au particles. Au particles were also seen along the plasma membrane of the oocytes and within the perivitelline space. The zona pellucida was not labeled by hyaluronidase Au. Different control expts. confirmed the specificity of the labeling. Digestion of thin sections with hyaluronidase prior to incubation with hyaluronidase-Au abolished the initial reaction, whereas treatment of thin sections with chondroitinase did not prevent labeling of oocyte-cumulus

complexes by hyaluronidase-Au. Although the function of hyaluronic acid in the oocyte-cumulus complex at the time of ovulation and fertilization is not known, the high concn. of this particular compd. in the cumulus matrix and the cumulus cells and its specific locations in the perivitelline space and in the superovulated oocytes implicate the significance of its presence and warrant future investigations.

L26 ANSWER 118 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1990:230910 CAPLUS <<LOGINID::20080906>>
DN 112:230910
OREF 112:38819a,38822a
TI 3,4,3',4'-Tetrachlorobiphenyl distribution and induced effects in the rat adrenal gland. Localization in the zona fasciculata
AU Durham, Stephen K.; Brouwer, Abraham
CS Dep. Toxicol. Pathol., Hoffmann-La Roche, Nutley, NJ, 07110, USA
SO Laboratory Investigation (1990), 62(2), 232-9 CODEN: LAINAW; ISSN: 0023-6837
DT Journal
LA English
AB The distribution of radiolabeled 3,4,3',4'-tetrachlorobiphenyl (TCB) and TCB-induced effects on serum and adrenal gland retinoid content, and adrenal gland morphol. was studied by liq. scintillation counting HPLC, light microscopic autoradiog., and TEM. Adult, female WAG/Rij rats received a single i.p. injection of either vehicle (corn oil), 15 mg TCB/kg, or 200 mg TCB/kg and were sacrificed at 1, 3, 7, and 14 days after treatment. One rat of the high-dose group that was sacrificed at each sampling time had received radiolabeled compd. (contg. 1.85 mCi of [3H]TCB). At day 1, the adrenal gland had the greatest concn. of radioactivity of any organ examd. There was a selective distribution of radiolabeled compd. to the zona fasciculata accompanied by morphometric evidence of hypertrophy of the zona fasciculata. The majority of [3H]TCB present in the adrenal gland was parent compd. at all time periods. Serum retinol content was decreased in the high-dose group by 61 and 54% at days 3 and 7, resp. No decrease in adrenal gland retinoid content occurred at any time in this study, but in contrast, adrenal gland retinol and retinyl palmitate content was increased. Serum cortisol levels were transiently decreased in the high-dose group. Ultrastructural alterations were only obsd. in cells of the zona fasciculata. Predominant changes included ***mitochondrial*** hypertrophy and concentric whorling lamellar ***arrays*** of the membranes of the outer ***mitochondrial*** compartment and ***mitochondrial*** cristae. Thus, the rat adrenal gland is an early target organ after TCB intoxication; there is an early and selective distribution of TCB in the rat adrenal gland accompanied by morphol. alterations in the sites of compd. localization. The obsd. morphol. changes apparently are not the result of hypovitaminosis A.

L26 ANSWER 119 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1990:152616 CAPLUS <<LOGINID::20080906>>
DN 112:152616
OREF 112:25651a,25654a
TI Sequences similar to genes for two ***mitochondrial*** proteins and portions of ribosomal RNA in tandemly ***arrayed*** 6-kilobase-pair DNA of a malarial parasite
AU Vaidya, Akhil B.; Akella, Rama; Suplick, Kathleen
CS Dep. Microbiol. Immunol., Hahnemann Univ., Philadelphia, PA, 19102-1192, USA
SO Molecular and Biochemical Parasitology (1989), 35(2), 97-107 CODEN: MBIPDP; ISSN: 0166-6851
DT Journal
LA English
AB Erythrocytic stages of mammalian malarial parasites contain acristate mitochondria whose functions are not well understood. Moreover, little is known about the genome of these organelles. It has been previously reported that all species of malarial parasites examd. contain highly conserved, tandemly arrayed DNA with a unit length of about 6.0 kb that is transcribed into discrete RNA mols. in erythrocytic stages. This report presents the complete DNA sequence of the 5984-bp repeating unit of Plasmodium yoelii, a rodent parasite. Two slightly overlapping regions transcribed into large RNA mols. were found to have significant DNA and protein sequence similarity with mitochondrion-coded protein, cytochrome c oxidase subunit I and cytochrome b. Significant sequence similarity with other mitochondrial protein genes could not be detected. Genes encoding rRNA were not detected in this sequence either. However, 2 regions, 82 and 50 nucleotides long, specified by different strands, were found to have extensive similarity with the highly conserved central loop of the peptidyl transferase domain of the large rRNA of Escherichia coli, mitochondria, and chloroplasts. Compensatory nucleotide substitutions were present in these regions, so that the predicted secondary structure was not affected. Functional utilization of these regions, if it exists, could argue for a trans-associative origin of rRNA. In organization, size and sequence, the tandem arrays of 6.0 kb malarial DNA appear to be a very unusual form of mitochondrial DNA.

L26 ANSWER 120 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1989:547827 CAPLUS <<LOGINID::20080906>>
DN 111:147827
OREF 111:24557a,24560a
TI Putative target sites for mobile G + C rich clusters in yeast ***mitochondrial*** DNA: single elements and tandem ***arrays***
AU Weiller, Georg; Schueller, Christine M. E.; Schweyen, Rudolf J.
CS Inst. Genet. Mikrobiol., Univ. Munich, Munich, D-8000/19, Fed. Rep. Ger.
SO Molecular and General Genetics (1989), 218(2), 272-83 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB GC clusters constitute the major repetitive elements in the mitochondrial (mt) genome of the yeast Saccharomyces cerevisiae. Many of these clusters are optional and thus contribute much to the polymorphism of yeast mtDNAs. A systematic search for polymorphic sites was undertaken by comparing mtDNA sequences of various yeast strains. Most of the 26 di- or polymorphic sites found differ by the presence or absence of a GC cluster of the major class, here referred to ass the M class, which terminate with an AGGAG motif. Comparison of sequences with and without the GC clusters reveal that elements of the subclasses M1 and M2 are inserted 3' to a TAG, flanked by a A + T rich sequences. M3 elements, in contrast, only occur in tandem arrays of 2 to 4 GC clusters; they are consistently inserted 3' to the AGGAG terminal sequence of a preexisting cluster. The TAG or the terminal AGGAG, therefore, are regarded as being part of the target sites for M1 and M2 or M3 elements, resp. The dinucleotide AG is in common to both target sites; it also occurs at the 3' terminus (AGGAG). This suggests its duplication during GC cluster insertion. This notion is supported by the observation that GC clusters of the minor

classes G and V similarly repeat at their 3' terminus a GT or an AA dinucleotide, resp., from their putative target sites.

L26 ANSWER 121 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1988:200523 CAPLUS <<LOGINID::20080906>>
DN 108:200523
OREF 108:32845a,32848a
TI Lateral segregation of sterol and channel proteins in the mitochondrial outer membrane induced by phospholipase A2: evidence from negative-stain electron microscopy using filipin
AU Mannella, Carmen A.
CS Sch. Public Health, State Univ. New York, Albany, NY, 12201, USA
SO Journal of Ultrastructure and Molecular Structure Research (1988), 98(2), 212-16 CODEN: JUMREG; ISSN: 0889-1605
DT Journal
LA English
AB The channel protein in the ***mitochondrial*** outer membrane of Neurospora crassa aggregates laterally into cryst. ***arrays*** by the action of phospholipase A2. When mitochondrial outer membranes are reacted with filipin and examd. by neg.-stain electron microscopy, filipin-sterol complexes are found everywhere on the membranes except on the cryst. channel arrays. Thus, the channel-rich membrane domains may have a relatively low content of accessible sterol. The in vitro segregation of protein and lipid membrane components by phospholipase A2 may reflect a mechanism by which the endogenous enzyme organizes the native mitochondrial membrane into functional domains.

L26 ANSWER 122 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1987:171503 CAPLUS <<LOGINID::20080906>>
DN 106:171503
OREF 106:27764h,27765a
TI Cytochrome c binds to lipid domains in ***arrays*** of ***mitochondrial*** outer membrane channels
AU Mannella, Carmen A.; Ribeiro, Agostinho J.; Frank, Joachim
CS Wadsworth Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Biophysical Journal (1987), 51(2), 221-6 CODEN: BIOJAU; ISSN: 0006-3495
DT Journal
LA English
AB Computer-averaged electron microscopic images of neg. stained cryst. ***arrays*** of fungal ***mitochondrial*** outer-membrane channels in the presence and absence of cytochrome c were compared. Neither the apo nor the holo-forms of cytochrome c significantly changed the stain distribution in the protein regions of the channel arrays. However, both forms of cytochrome c caused significant stain exclusion from the lipid domains in the arrays, suggesting binding of the polypeptides at these loci. The implications of binding of apocytochrome c to clusters of exposed phospholipids on the mitochondrial outer membrane are discussed with respect to the mechanism of uptake of this polypeptide by mitochondria.

L26 ANSWER 123 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1986:475128 CAPLUS <<LOGINID::20080906>>
DN 105:75128
OREF 105:12141a,12144a
TI Mitochondrial outer membrane channel (VDAC, porin) two-dimensional crystals from Neurospora
AU Mannella, Carmen A.
CS Wadsworth Cent., New York State Dep. Health, Albany, NY, 12201, USA
SO Methods in Enzymology (1986), 125(Biomembranes, Pt. M), 595-610 CODEN: MENZAU; ISSN: 0076-6879
DT Journal; General Review
LA English
AB A review with 38 refs. Cryst. ***arrays*** of ***mitochondrial*** channels are induced by dialysis in the presence of phospholipase A2, after isolation of mitochondrial outer membranes. The arrays of porins and voltage-dependent, anion-selective channels (VDAC) can be studied by neg. stain-electron microscopy.

L26 ANSWER 124 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1986:125295 CAPLUS <<LOGINID::20080906>>
DN 104:125295
OREF 104:19723a,19726a
TI Structure of the channels in the outer ***mitochondrial*** membrane. Electron microscopic studies of the periodic ***arrays*** induced by phospholipase A2 treatment of the Neurospora membrane
AU Mannella, C. A.; Ribeiro, A.; Frank, J.
CS Wadsworth Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Biophysical Journal (1986), 49(1), 307-18 CODEN: BIOJAU; ISSN: 0006-3495
DT Journal
LA English
AB The channel proteins in outer membranes of N. crassa ***mitochondria*** spontaneously organize into periodic ***arrays*** when the membranes are dialyzed in the presence of sol. phospholipase A2. Electron microscopic images were recorded at different electron doses from channel arrays in a variety of neg. strains, as well as in vitreous ice. Fourier or correlation avs. are formed from image fields contg. a few hundred unit cells. These avs. can be subsequently classified by correspondence anal. and summed to form representative avs. over thousands of unit cells. In avs. of neg. stained arrays, the stain-filled channel openings are bounded by smaller stain-excluding max. The projections of the channel openings are smaller and the subsidiary max. are more pronounced for channel arrays contrasted with dil. (0.1%) uranyl acetate or aurothioglucose than for arrays embedded in 1% uranyl acetate. Projection images of unstained, ice-embedded membranes provide direct information about distribution of protein and lipid in the voltage-dependent, anion-selective channel arrays. First expts. have yield d. maps with an apparent Fourier resoln. of .apprx.1/(2 nm).

L26 ANSWER 125 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1985:108141 CAPLUS <<LOGINID::20080906>>
DN 102:108141
OREF 102:16911a,16914a
TI Physical basis for the maternal inheritance of triazine resistance in Amaranthus hybridus
AU Vaughn, K. C.
CS South. Weed Sci. Lab., USDA, Stoneville, MS, 38776, USA
SO Weed Research (1985), 25(1), 15-19 CODEN: WEREAT; ISSN: 0043-1737
DT Journal
LA English
AB To det. the phys. basis of the maternal inheritance of triazine resistance in A. hybridus the fate of plastids and other organelles in developing pollen was investigated in triazine-

resistant and susceptible biotypes. In both types, immediately after microspore mitosis, the newly formed generative cells contained an ***array*** of organelles (golgi bodies, endoplasmic reticulum, plastids and ***mitochondria***) similar to that in the larger vegetative cells. No selective exclusion of organelles from the generative cell was noted although only small plastids were present. The immature generative cells contained small vacuoles, within which degenerate organelles were frequently obsd., and no ultrastructurally recognizable plastids were found in mature cells. Maternal transmission of the triazine resistance factor thus appears to be due to a selective destruction of paternal plastids.

L26 ANSWER 126 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1984:626124 CAPLUS <<LOGINID::20080906>>
DN 101:226124
OREF 101:34247a,34250a
TI Negative staining characteristics of ***arrays*** of ***mitochondrial*** pore protein: use of correspondence analysis to classify different staining patterns
AU Mannella, Carmen A.; Frank, Joachim
CS Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Ultramicroscopy (1984), 13(1-2), 93-102 CODEN: ULTRD6; ISSN: 0304-3991
DT Journal
LA English
AB Fourier-filtered electron microscopic images of neg. stained ***arrays*** of ***mitochondrial*** pore protein were classified by correspondence anal. of their diffraction patterns. The most significant component of interpattern variation is an isotropic shift in reflection intensities between high- and low-order reflections. This corresponds in the images to the presence or absence of high resoln. detail (stain min.). Exptl. the loss of detail in images correlates with the use of highly dissocd. heavy metal salts as neg. stains. It is proposed that such stains yield poorer neg.-contrast images due to electrostatic binding of heavy-metal complex ions to fixed charge groups on the protein. Results with surface-modified protein arrays are consistent with this hypothesis.

L26 ANSWER 127 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1984:607460 CAPLUS <<LOGINID::20080906>>
DN 101:207460
OREF 101:31375a,31378a
TI Fluorescence microscopic studies of mitochondrial nucleoids during meiosis and sporulation in the yeast, Saccharomyces cerevisiae
AU Miyakawa, Isamu; Aoi, Hiroyuki; Sando, Nobundo; Kuroiwa, Tsuneyoshi
CS Fac. Sci., Yamaguchi Univ., Yamaguchi, 753, Japan
SO Journal of Cell Science (1984), 66, 21-38 CODEN: JNCSAI; ISSN: 0021-9533
DT Journal
LA English
AB Configurational changes of mitochondria and mitochondrial nucleoids (mt-nucleoids) during meiosis and sporulation in the yeast, S. cerevisiae, were examd. by using the mitochondrial membrane-binding fluorescent dye, di-Me aminostyrylmethylpyridinium iodine (DASPMI) and the DNA-binding fluorescent dye, 4',6-diamidino-2-phenylindole (DAPI). In zygotes just after mating, mt-nucleoids were obsd. as many small discrete light spots in the cytoplasm. During meiosis in zygotes, mt-nucleoids at first coalesced with each other into a long string and then sepd. into spherical nucleoids in 4 spores. These changes paralleled those in mitochondria obsd. using DASPMI. The use of spheroplasts allowed one to examine the behavior of mt-nucleoids at higher resoln. and to identify several distinct meiotic prophase stages of the cell nucleus during early sporulation. In diploid spheroplasts at the stationary phase, 50-70 of the mt-nucleoids were sepd. from each other and each spherical mitochondrion contained only one mt-nucleoid. At the later stage of premeiotic DNA synthesis, a single branched giant mitochondrion was formed as a result of complete mitochondrial fusion. All of the mt-nucleoids were arranged in an ***array*** on a giant ***mitochondrion*** and coalesced into a string-like network. Through meiosis I and II, strings of mt-nucleoids were obsd. close to the dividing nuclei. At late meiosis II, a ring of mt-nucleoids enclosing each daughter nucleus was formed. In ascospores, discrete small nucleoids were visible close to each spore nucleus with a string-of-beads appearance. Many mt-nucleoids were excluded from the ascospores and remained in the residual cytoplasm of the ascus.

L26 ANSWER 128 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1984:505989 CAPLUS <<LOGINID::20080906>>
DN 101:105989
OREF 101:16109a,16112a
TI Evidence that the crystalline ***arrays*** in the outer membrane of Neurospora ***mitochondria*** are composed of the voltage-dependent channel protein
AU Mannella, Carmen A.; Colombini, Marco
CS Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Biochimica et Biophysica Acta, Biomembranes (1984), 774(2), 206-14 CODEN: BBBMBS; ISSN: 0005-2736
DT Journal
LA English
AB Antibodies specific for the major polypeptide (mol. wt., Mr 31,000) of the outer membrane of Neurospora mitochondria and its slower-migrating derivs. on SDS-polyacrylamide gels were raised in rabbits. These antibodies inhibited the insertion into phospholipid bilayers of voltage-dependent ion channels from detergent exts. of the mitochondrial outer membranes. The same antibodies bound preferentially to outer ***mitochondrial*** membrane fractions contg. cryst. surface ***arrays*** . The Mr-31,000 polypeptide is a component both of the ion channels and of the membrane arrays, suggesting identity between the functional and structural entities.

L26 ANSWER 129 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1983:536720 CAPLUS <<LOGINID::20080906>>
DN 99:136720
OREF 99:20969a,20972a
TI pif Mutation blocks recombination between ***mitochondrial*** .rho.+ and .rho.- genomes having tandemly ***arrayed*** repeat units in Saccharomyces cerevisiae
AU Foury, Francoise; Kolodynski, Jan
CS Univ. Louvain, Louvain-la-Neuve, 1348, Belg.
SO Proceedings of the National Academy of Sciences of the United States of America (1983), 80(17), 5345-9 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Three allelic nuclear mutants affected in the recombination of mitochondrial (mt)DNA were characterized in S. cerevisiae and assigned to the PIF locus. In the mutants, the general

recombination measured by the recombination frequency between linked or unlinked alleles is normal. However, the pif mutations prevent the integration into the .rho.+ genome of the markers (oli1, oli2, diu1, ery, oxi1, oxi2) of those .rho.- genomes that have tandemly arrayed repeat units. Therefore, these .rho.- genomes characterize a PIF-dependent recombination system. The pif mutations have also revealed the existence of a PIF-independent recombination system used by those .rho.- genomes that have an inverted organization of their repeat units. The markers of such palindromic .rho.- genomes exhibit high integration frequency into the .rho.+ genome even in the presence of the pif mutation. In addn., the pif mutations greatly increase suppressiveness in crosses between pif .rho.+ strains and PIF-dependent as well as PIF-independent .rho.- clones. Apparently the recombination between .rho.+ and .rho.- genomes involves .gtoreq.2 distinct systems that depend on the organization of the .rho.- genome.

L26 ANSWER 130 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1983:434786 CAPLUS <<LOGINID::20080906>>
DN 99:34786
OREF 99:5429a,5432a
TI Structural and functional evidence for multiple channel complexes in the outer membrane of Neurospora crassa mitochondria
AU Mannella, Carmen A.; Colombini, Marco; Frank, Joachim
CS Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1983), 80(8), 2243-7 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The outer membrane of mitochondria contains proteins that form channels called VDAC (voltage-dependent anion-selective channels). Two independent lines of evidence suggest that these channels occur in specific complexes in the outer membrane of Neurospora mitochondria. Electron microscopic images of these outer membranes reveal polymorphic cryst. arrays of putative pores. These arrays are interrelated by movement in the membrane plane of a particular rigid channel triplet or of regular aggregates of this triplet. Detergent exts. of the same outer membranes induce single- and multiple-step conductances in planar phospholipid membranes, with a marked preference for the insertion of triplets and multiples of triplets. The tendency of the ***mitochondrial*** channels to occur as extended ***arrays*** , apparently built up from triplets, may have important functional and evolutionary implications.

L26 ANSWER 131 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1983:401348 CAPLUS <<LOGINID::20080906>>
DN 99:1348
OREF 99:287a,290a
TI Liver morphology in guinea pigs administered either pyrolysis products of a polychlorinated biphenyl transformer fluid or 2,3,7,8-tetrachlorodibenzo- p-dioxin
AU Turner, J. N.; Collins, D. N.
CS Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Toxicology and Applied Pharmacology (1983), 67(3), 417-29 CODEN: TXAPA9; ISSN: 0041-008X
DT Journal
LA English
AB A transformer cooled and insulated with a mixt. of 65% Aroclor 1254 and 35% chlorinated benzenes was involved in a fire, which produced soot contg. polychlorinated biphenyls, biphenylenes, dioxins, and dibenzofurans. A single dose of either soot or 2,3,7,8-tetrachlorodibenzo- p-dioxin (I) [1746-01-6] in aq. Me cellulose was administered by gavage to Hartley guinea pisg of both sexes. The liver tissue was examd. 42 days after administration. By light microscopy hypertrophy of hepatocytes, steatosis, focal necrosis, and cytoplasmic hyalin-like bodies were obsd. as a result of both treatments. Bile duct proliferation (adenofibrosis) was obsd. only in the guinea pig groups administered soot. These animals also showed proliferation of the smooth endoplasmic reticulum, concentric membrane ***arrays*** (CMA), ***mitochondrial*** alterations, decreased rough endoplasmic reticulum, and autophagolysosomes by electron microscopy. The CMAs, which corresponded to the hyalin-like bodies, surrounded lipid droplets and cytoplasmic matrix contg. mitochondria and degenerating organelles.

L26 ANSWER 132 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1983:401336 CAPLUS <<LOGINID::20080906>>
DN 99:1336
OREF 99:286h,287a
TI Structural alterations of nerve cell in experimental acute tetraethyllead poisoning on rats
AU Akai, Keiichiro; Yamada, Kazuaki; Uchigasaki, Shinya; Kawaguchi, Reiko; Watanabe, Kazumi; Kawamori, Masao; Matsui, Tomoko; Matsumoto, Kazuya
CS Sch. Med., Kyorin Univ., Mitaka, 181, Japan
SO Kyorin Igakkai Zasshi (1982), 13(3), 303-13 CODEN: KIZSB8; ISSN: 0368-5829
DT Journal
LA Japanese
AB Histopathol. changes were studied on nerve cells of rats given 10, 20, 40, 60, and 80 mg/kg Et4Pb [78-00-2] i.p. for 2-7 days. The light microscopic examn. revealed extensive hydropic degeneration of nerve cells in the cerebrum, cerebellum, and spinal cord. The most significant feature was selective necrosis of the nerve cells in the hippocampus treated with >20 mg/kg Et4Pb. On electromicroscopic examn., the affected nerve cells initially demonstrated an increased no. of mitochondria which were remarkably swollen, lysosomes, and multivesicular bodies; in addn., considerable enlargement of the Golgi complexes and rough endoplasmic reticula were noted. As these processes progressed, some nerve cells showed a remarkable decrease in the no. of mitochondria and contained a large no. of round cytoplasmic vacuoles surrounded by a single membrane with no structural content and numerous collections of electron dense bodies consisting of degenerated ***mitochondria*** , multimembranous bodies, and autophagic vacuoles with some membranous ***arrays*** . The subcellular manifestation of nerve cells undergoing mitochondrial swelling and hydropic degeneration with sequential changes to formation of dense bodies exhibited a distinct pattern. Thus, Et4Pb poisoning had deleterious and selective effects on the cellular and subcellular components in certain parts of the brain.

L26 ANSWER 133 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1982:540609 CAPLUS <<LOGINID::20080906>>
DN 97:140609
OREF 97:23335a,23338a

TI Structure of the outer ***mitochondrial*** membrane: ordered ***arrays*** of porelike subunits in outer-membrane fractions from Neurospora crassa ***mitochondria***
AU Mannella, Carmen A.
CS Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201, USA
SO Journal of Cell Biology (1982), 94(3), 680-7 CODEN: JCLBA3; ISSN: 0021-9525
DT Journal
LA English
AB Light-membrane fractions obtained by hypoosmotic lysis of N. crassa mitochondria exhibit buoyant densities and marker-enzyme activities characteristic of outer mitochondrial membranes. SDS-polyacrylamide gel electrophoresis of these membrane fractions indicates that a polypeptide of relative mol. wt. 31,000 is the main protein component. Under neg.-stain electron microscope examn. many of the membranes in these fractions appear as large (0.5-1 .mu.m diam.), collapsed vesicles. The surfaces of flattened, open (i.e., ripped) vesicles often exhibit extended 2-dimensional arrays of subunits with central, 2-3-nm diam., stain-accumulating sites. These porelike subunits are arranged into hexagons within each parallelogram unit cell, 12.6 .times. 11.1 nm (lattice angle = 109.degree.).

L26 ANSWER 134 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1982:1907 CAPLUS <<LOGINID::20080906>>
DN 96:1907
OREF 96:347a,350a
TI Mitochondrial anomalies in renal oncocytes induced in the rat by N-nitrosomorpholine
AU Krech, Rainer; Zerban, Heide; Bannasch, Peter
CS Inst. Exp. Pathol., Deutsches Krebsorschungszent., Heidelberg, D-6900/1, Fed. Rep. Ger.
SO European Journal of Cell Biology (1981), 25(2), 331-9 CODEN: EJCBDN; ISSN: 0171-9335
DT Journal
LA English
AB Renal oncocytes were induced in male rats by oral application of N-nitrosomorpholine (NNM) [59-89-2] in 12 or 50 mg/100 mL drinking water and analyzed by transmission electron microscopy. The oncocytes exhibited mitochondrial anomalies which were very similar to those of human oncocytoma oncocytes. The most striking mitochondrial changes were an unusually large no. of the organelles and an excess of the mitochondrial cristae. The shape of the mitochondria varied from round and oval to extremely elongated slender or cup-shaped organelles often piled up to form complex bodies. Rarely large ramifying mitochondria were found. In addn. to transversely oriented cristae or tubules, the inner mitochondrial membranes frequently formed dense stacks of unusually long cristae often arranged longitudinally. In some mitochondria, straight and strictly parallelly arranged neighboring cristae were connected by a paracryst. ***array*** of pillars bridging the ***mitochondrial*** matrix. In the majority of oncocytes, the mitochondrial matrix contained prominent dense granules (diam. 30-50 nm), but sometimes these were rare or absent. Individual mitochondria of many oncocytes showed membrane-bound deposits of glycogen particles which usually formed rosettes (.alpha.-particles) with a diam. of .apprx.80 nm. Partitioned mitochondria were not seen. Often autophagic vacuoles contg. portions of degraded mitochondria and dense bodies, probably autophagosomes, were obsd. The nature and significance of the oncocytes remains unclear. Apparently, oncocytes represent a special type of a neoplastically transformed cell which usually has only a low potential for autonomous growth. Renal oncocytes induced in rats by chem. carcinogens appear to be an excellent exptl. model for the further investigation of this cell type.

L26 ANSWER 135 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1981:137136 CAPLUS <<LOGINID::20080906>>
DN 94:137136
OREF 94:22443a,22446a
TI The identification of calmodulin-binding sites on mitochondria in cultured 3T3 cells
AU Pardue, Robert L.; Kaetzel, Marcia A.; Hahn, Stephen H.; Brinkley, B. R.; Dedman, John R.
CS Dep. Cell Biol., Baylor Coll. Med., Houston, TX, 77030, USA
SO Cell (Cambridge, MA, United States) (1981), 23(2), 533-42 CODEN: CELLB5; ISSN: 0092-8674
DT Journal
LA English
AB Calmodulin was uniformly labeled with tetra-Me rhodamine isothiocyanate (CaM-RITC) and the deriv. was used as a mol. probe to identify available, unoccupied calmodulin-binding sites. In mildly fixed (3% formalin) cultured 3T3 cells, the biol. active CaM-RITC bound predominantly to mitochondria. Binding was markedly decreased in the presence of 1 mM EGTA. Stelazine, a phenothiozine which binds to calmodulin, prevented the interaction of CaM-RITC with mitochondrial sites. A 10-fold excess of unlabeled calmodulin competitively inhibited binding. Fluorescently labeled troponin C and parvalbumin did not bind to mitochondria on any other cellular organelle. Rhodamine alone did not bind to 3T3 mitochondria. Similar results were obtained using [125I]calmodulin binding to isolated rat liver mitochondria. When solubilized mitochondrial proteins were subjected to calmodulin-Sepharose affinity chromatog. and eluted with 1 mM EGTA, there were 2 major polypeptides 120,000 and 67,000 daltons and at least 3 minor species (100,000, 60,000 and 40,000 daltons). The interaction required an active Ca2+-calmodulin complex and was specific for calmodulin. Double fluorescent staining with CaM-RITC and fluorescein-labeled antibodies to tubulin and DNAase I revealed a ***mitochondrial*** distribution pattern similar to that of microtubule ***arrays*** but unrelated to actin cabling. There was no evidence that CaM-RITC directly interacted with either microtubules or microfilaments.

L26 ANSWER 136 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1980:598786 CAPLUS <<LOGINID::20080906>>
DN 93:198786
OREF 93:31603a,31606a
TI The presence of hepatic intramitochondrial crystalline inclusions in polybrominated biphenyl-treated mice
AU Wilson-Martino, Nancy A.; Martino, Leon J.; Millman-Feder, Nancy G.; Benitz, Karl F.
CS Inst. Exp. Pathol. Toxicol., Albany Med. Coll., Albany, NY, 12208, USA
SO Archives of Toxicology (1980), 45(3), 233-9 CODEN: ARTODN; ISSN: 0340-5761
DT Journal
LA English
AB Electron microscopic study of livers from mice fed 167 ppm polybrominated biphenyl revealed mitochondrial abnormalities which consisted of both alterations in size and the formation of cryst.-like inclusions within the mitochondrial matrix. These inclusions appeared as parallel ***arrays*** of rods and were found in elongated ***mitochondria*** which contained few cristae. The significance of such inclusions in relation to mitochondrial aberrations is discussed.

L26 ANSWER 137 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1980:174350 CAPLUS <<LOGINID::20080906>>
DN 92:174350
OREF 92:28115a,28118a
TI Effect of 10-hydroxycamptothecin on the ultrastructure of ascitic hepatoma cells in mice
AU Wang, Zu-Wu; Shu, Rong-Sen; Xu, Bin
CS Shanghai Inst. Mater. Med., Acad. Sin., Shanghai, Peop. Rep. China
SO Zhonghua Zhongliu Zazhi (1979), 1(3), 183-5 CODEN: CCLCDY; ISSN: 0253-3766
DT Journal
LA Chinese
AB 10-Hydroxycamptothecin (I) [67656-30-8](10 or 20 mg/kg, i.p.) reduced the electron d. of nuclear matrices (including chromatin and nucleoli), caused ***mitochondrial*** swelling with an irregular ***array*** and even obscurity and disappearance of inner cristae, caused marked dilation of the Golgi app. cisternae and to a lesser extent the endoplasmic reticulum, increased vacuoles, lipid droplets, and lysosomes, and caused scattered interruptions of the plasmalemma and nuclear envelope in hepatoma cells and hepatocytes of mice bearing ascitic hepatoma 2 and 6 h after treatment. I dose and time of exposure affected the extent of the above changes. Inhibitory effects on nucleic acids may be involved in the I activity.

L26 ANSWER 138 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1979:148826 CAPLUS <<LOGINID::20080906>>
DN 90:148826
OREF 90:23637a,23640a
TI Cyclic development of the smooth endoplasmic reticulum in thoracic glands (ecdysial glands) of Rhodnius prolixus Stal (Insecta: Heteroptera) during the two last larval instars
AU Gras, R.; Beaulaton, J.
CS Groupe Zool., Univ. Clermont II, Aubiere, Fr.
SO Experientia (1979), 35(3), 386-8 CODEN: EXPEAM; ISSN: 0014-4754
DT Journal
LA French
AB An ultrastructural study of the thoracic glands of R. prolixus during the last 2 larval instars demonstrated the cyclic differentiation of meshed networks of smooth endoplasmic reticulum. At abdominal apolysis, the ecdysial cells were compartmentalized into a peripheral ***array*** of smooth endoplasmic reticulum with sparse ***mitochondria*** . The close assocn. of smooth endoplasmic reticulum and mitochondria may indicate functional coupling with respect to ecdysone formation.

L26 ANSWER 139 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1977:402119 CAPLUS <<LOGINID::20080906>>
DN 87:2119
OREF 87:371a
TI Purification and characterization of a virus associated with the grapevine leafroll disease
AU Tanne, Edna; Sela, I.; Klein, M.; Harpaz, I.
CS Volcani Cent., Agric. Res. Organ., Bet Dagan, Israel
SO Phytopathology (1977), 67(4), 442-7 CODEN: PHYTAJ; ISSN: 0031-949X
DT Journal
LA English
AB Grape leafroll virus (GLRV) which is assocd. with the leafroll disease in grapevine, and also is transmissible to herbaceous plants, was purified from Nicotiana glutinosa and Datura metel and characterized. Flexuous, rod-shaped, infectious virus particles were found. They were heterogeneous in size due to fragility and aggregation. The sedimentation coeff. of the normal-size particle (13 .times. 790 nm) was .apprx. 150 S. The virus formed a single band at 1.32 g/cm3 upon CsCl equil. centrifugation. The mol. wt. of GLRV-RNA was estd. as 2.9-3.5 .times. 106. A single protein band, 31,000 daltons in mol. wt., was detected upon polyacrylamide gel electrophoresis of purified GLRV in the presence of Na dodecyl sulfate or urea. A variety of inclusion bodies and abnormal structures were obsd. in ultrathin sections of N. glutinosa and D. metel. These included pinwheeles, bundles of filaments, ***arrays*** of cryst. matter, and giant ***mitochondria*** . Grape leafroll virus is classified in the potyvirus group.

L26 ANSWER 140 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1976:539825 CAPLUS <<LOGINID::20080906>>
DN 85:139825
OREF 85:22415a,22418a
TI Phytochrome-mediated development of mitochondria in the cotyledons of mustard (Sinapis alba L.) seedlings
AU Bajracharya, D.; Falk, H.; Schopfer, P.
CS Biol. Inst. II, Univ. Freiburg, Freiburg/Br., Fed. Rep. Ger.
SO Planta (1976), 131(3), 253-61 CODEN: PLANAB; ISSN: 0032-0935
DT Journal
LA English
AB The development of mitochondria from promitochondria is regulated by phytochrome. This conclusion is based on: (1) the activity of representative mitochondria marker enzymes (fumarase, succinate dehydrogenase, cytochrome oxidase) was increased by continuous far-red light and (in 2 of the 3 enzymes) by brief red pulses, the effect of which was reversible by far-red pulses; these effects did not merely represent a general growth or proliferation of mitochondria already present but specific responses of individual enzymes; inhibitors of protein synthesis but not of RNA synthesis suppressed the increase of these enzyme activities; (2) continuous far-red light changedsome structural properties of the mitochondrial membranes, detectable by an increased requirement of detergent (Triton X-100) for the solubilization of cytochrome oxidase and a more efficient retainment of the matrix enzyme fumarase during isolation of mitochondria; (3) continuous far-red light had a strong effect on the morphol. of the inner ***mitochondrial*** membrane system; electron micrographs from dark-grown cotyledons showed ***arrays*** of parallel, plate-like cristae while typical plant ***mitochondria*** with irregularly oriented sacculi were formed in the light. These responses indicate the involvement of mitochondria in cytophotomorphogenesis during the transition of the cotyledons from dissimilatory to assimilatory metab.

L26 ANSWER 141 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1975:55697 CAPLUS <<LOGINID::20080906>>
DN 82:55697
OREF 82:8915a,8918a
TI Carcinoplacental isoenzymes. Ultrastructural studies in ovarian cancer and Regan and non-Regan isoenzyme producing HeLa cell lines
AU Fishman, William H.; Sasaki, Mitsuo; Singer, Robert M.
CS Sch. Med., Tufts Univ., Boston, MA, USA

SO Tumor Research (1973), 8, 135-45 CODEN: TUREA6; ISSN: 0041-4093
DT Journal
LA English
AB The carcinoplacental isoenzymes represent a subgroup of carcinoplacental proteins. Along with carcinofetal and carcinofetalplacental proteins these 3 subgroups belong under the term carcinoembryonic proteins. Accordingly in this classification, it was possible to retain an anatomic basis of ref. in terms of the whole process of development. Untrastructural studies on the sites of alk. phosphatase in human ovarian cancer cells revealed an apparent assocn. of Regan isoenzyme with mitochondrial membranes and of non-Regan isoenzyme with cell surface membranes. The origin of the mitochondrial enzyme is unknown. Interesting ***arrays*** of ***mitochondria*** enveloped partially or entirely by endoplasmic reticulum exhibited ribosomes on the membranes facing the mitochondria were obsd. These arrays were indistiguishable from those obsd. in cytotrophoblastic cells of the placenta.

L26 ANSWER 142 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1974:489345 CAPLUS <<LOGINID::20080906>>
DN 81:89345
OREF 81:14171a,14174a
TI Mitochondrial synthesis of glycoproteins and surface properties of mitochondrial membranes
AU Bosmann, H. Bruce; Myers, M. W.
CS Sch. Med. Dent., Univ. Rochester, Rochester, NY, USA
SO Biogenesis Mitochondria, Proc. Int. Conf. (1974), Meeting Date 1973, 525-36. Editor(s): Kroon, A. M. Publisher: Academic, New York, N. Y. CODEN: 28JQAB
DT Conference
LA English
AB Several neoplastic model cells were studied to det. the nature of autonomous mitochondrial glycoprotein synthesis. Labeled monosaccharide was transferred onto both endogenous and exogenous acceptor proteins by enzyme sources prepd. from hepatoma and host liver mitochondria. Hepatoma mitochondria showed greater transfer onto exogenous acceptors than liver mitochondria, indicating high transferase activity. When exogenous acceptors were omitted, more monosaccharide was also incorporated by hepatoma mitochondria onto exogenous proteins. Polyacrylamide gel electrophoresis of ***mitochondrial*** proteins showed that the hepatoma ***mitochondria*** had an altered ***array*** of proteins. Electrophoretic mobility of whole hepatoma mitochondria toward the anode was greater than that of liver mitochondria, probably caused by its higher sialic acid content. These differences in mitochondria of normal and neoplastic cellsare complex and not clear-cut.

L26 ANSWER 143 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1974:423993 CAPLUS <<LOGINID::20080906>>
DN 81:23993
OREF 81:3893a,3896a
TI Carcinoplacental isoenzyme antigens
AU Fishman, William H.
CS Sch. Med., New England Med. Cent. Hosp., Boston, MA, USA
SO Advances in Enzyme Regulation (1973), 11, 293-321 CODEN: AEZRA2; ISSN: 0065-2571
DT Journal
LA English
AB A survey, with 158 refs., of catalytically active proteins present in tumors whose antigenic sites are identical to those of proteins present in the placenta but not in any fetal tissue. These were termed "carcinoplacental isoenzyme antigens," and afamily of placental isoenzymes of alk. phosphatase was presented as examples of such antigens. Evidence was presented indicating that normal phenotypes of placental alk. phosphatase were produced by tumors. In addn., electron micrographs of tumor tissue of an ovarian cancer patient showed sites of alk. phosphatase activity in the outer mitochondrial membranes, in the lateral cell borders and microvilli and in the dense-body type lysosomes. An ***array*** of ***mitochondria*** and endoplasmic reticulum resembling structures seen in placental cells was obsd. The evidence presented is consistent with current views that normal genes are active in cancer. It is suggested that activation of placental and fetal genes may play a role in malignancy and that epigenetic rather than mutational mechanisms apply.

L26 ANSWER 144 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1973:145434 CAPLUS <<LOGINID::20080906>>
DN 78:145434
OREF 78:23371a,23374a
TI Neurosecretory cells in the cerebral ganglion of adult tunicates. Fine structure and distribution of phosphatases
AU Lane, Nancy J.
CS Dep. Zool., Univ. Cambridge, Cambridge, UK
SO Journal of Ultrastructure Research (1972), 40(5-6), 480-97 CODEN: JULRA7; ISSN: 0022-5320
DT Journal
LA English
AB Adult Ciona, Styele, and Botryllus possessed a single cerebral ganglion, which consisted of a cortex of nerve cells surrounding a central neuropile. No glial investment was found for the neurons in these ganglia. The neuronal cytoplasm contained vesicles or cisternae of ribosome-studded endoplasmic reticulum which occasionally lay in parallel ***arrays*** or were extended around a ***mitochondrion*** . The Golgi saccules were probably the site of formation of the elementary neurosecretory granules by terminal budding. Both the lysosomes and the Golgi complexhad acid phosphatase (APase) nad thiamine pyrophosphatase (I) activities. The neurons of Styele and Ciona contained fewer and larger APase-pos.lysosomes than Botryllus. Some saccules and vesicles of the Golgi complex had both APase and I activities. The Golgi membrane around the immature neurosecretory gramules may show phosphatase activity, but the granules themselves did not. Some cisternae of the endoplasmic reticulum contained I. Neurons of the adult tunicates were cytol. more similar to the nerve cells of other invertebrate goups than to those of the vertebrates.

L26 ANSWER 145 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1973:94021 CAPLUS <<LOGINID::20080906>>
DN 78:94021
OREF 78:15039a,15042a
TI Paracrystalline ***arrays*** in ***mitochondria***
AU Korman, Ephraim F.; Harris, Robert A.; Williams, Charles H.; Wakabayashi, Takashi; Green, David E.; Valdivia, Enrique
CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, USA
SO Journal of Bioenergetics (1970), 1(4), 387-404 CODEN: JBEGAA; ISSN: 0449-5705
DT Journal
LA English
AB Evidence for the involvement and function of both intra- and extramitochondrial materials is discussed. Several examples of

paracryst. ***array*** patterns seen in ***mitochondria*** are presented.

L26 ANSWER 146 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1972:509691 CAPLUS <<LOGINID::20080906>>
DN 77:109691
OREF 77:18055a,18058a
TI Intramitochondrial lamellar formations induced by pregnenolone-16-.alpha.- carbonitrile in the hepatocytes of pregnant rats
AU Tuchweber, B.; Kovacs, K.; Khandekar, J. D.; Garg, B. D.
CS Inst. Med. Chirug. Exp., Univ. Montreal, Montreal, QC, Can.
SO Journal of Ultrastructure Research (1972), 39(5-6), 456-64 CODEN: JULRA7; ISSN: 0022-5320
DT Journal
LA English
AB Electron microscopic study of the livers of pregnant rats given pregnenolone-16.alpha.-carbonitrile (I) [1434-54-4] revealed mitochondrial abnormalities which comprised alterations in shape, increases in size, and formations of lamellar ***arrays*** within the ***mitochondrial*** matrix. These structures were 50-110 .ang. thick with a space of 160-200 .ang. between them and were found in the elongated mitochondria which contained a few cristae.

L26 ANSWER 147 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1972:429797 CAPLUS <<LOGINID::20080906>>
DN 77:29797
OREF 77:4945a,4948a
TI Cytotoxic effects of D-glucosamine on the ultrastructures of normal and neoplastic tissues in vivo
AU Molnar, Z.; Bekesi, J. G.
CS Dep. Pathol., Univ. Chicago, Chicago, IL, USA
SO Cancer Research (1972), 32(4), 756-65 CODEN: CNREA8; ISSN: 0008-5472
DT Journal
LA English
AB In rats bearing Walker tumors and infused with D-glucosamine [3416-24-8] (350 mg/kg/hr) for 40 hr, the nuclear matrix of the tumor cells showed a much-decreased electron d. and contained clumped interchromatin granules. The nucleoli had rounded up, and the strands of the nucleolonema had coalesced. The parenchymal cells of the liver showed almost complete fragmentation of the long profiles of the rough endoplasmic reticulum into small vesicles. Only small rows of the usual staggered ***array*** of cisternae remained surrounding ***mitochondria*** . Autophagic vacuoles were frequently seen. The lining epithelium of the proximal convoluted tubules of the kidney showed striking vesiculation of the cytoplasm. Necrosis of the liver or hepatic cells was not obsd. However, complete necrosis of tumor cells was obsd. in rats sacrificed 5 days after the infusion. This was accompanied by recovery of the fine structure of the renal and hepatic parenchymal cells.

L26 ANSWER 148 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1971:528723 CAPLUS <<LOGINID::20080906>>
DN 75:128723
OREF 75:20311a,20314a
TI Phenoxy acid-induced renal changes in the chicken. I. Ultrastructure
AU Bjorklund, Nils E.; Erne, Kurt
CS Dep. Pathol., R. Vet. Coll., Stockholm, Swed.
SO Acta Veterinaria Scandinavica (1971), 12(2), 243-56 CODEN: AVSCA7; ISSN: 0044-605X
DT Journal
LA English
AB Expts. confirmed that 2,4-D causes kidney enlargement in chickens due to hypertrophy of the tubular epithelium; the most spectacular changes were found in the proximal convoluted tubules. An attempt was made to elucidate, by means of electron microscopy, the nature of the renal changes induced in chickens by prolonged exposure to 2,4-D or 2,4,5-T. To 45-day-old broiler chickens a com. formulation of the triamine salt of 2,4-D or an aq. soln. of 2,4,5-T triethanolamine salt was given. The general condition of the treated chickens deteriorated; they became less agile and often sat with closed eyes. Food and water intake and growth rate were lowered; some died or were killed in a moribund state uring the first 4 weeks, general weakness being the sole clinical sign obsd. Gross tissue changes were obsd. mainly in the kidneys, with all receiving either chem. until death or sacrifice; the kidneys were spectacularly enlarged and had a pale appearance and firm consistency. The renal changes in the treated animals were of the same type, whether newly hatched or 8-week old birds were used and whether 2,4-D or 2,4,5-T was administered. The latter, however, generally evoked more profound changes. Ultrastructural changes were detectable already at the 1st sampling (after 14 days of exposure), the severity increasing with the exposure period. The most conspicuous changes were seen in the proximal convoluted tubules with notable changes in the nuclei and particularly in some of the cytoplasmic organelles. In the cytoplasm, changes were apparent in mitochondria and microbodies. Elongated ***mitochondria*** tended to form circular ***arrays*** enclosing various organelles. After extended exposure periods, mitochondria fused into more or less electron-opaque, structureless bodies appeared.

L26 ANSWER 149 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1970:10622 CAPLUS <<LOGINID::20080906>>
DN 72:10622
OREF 72:1910h,1911a
TI Comparative ultrastructural studies of glycogen-rich choroid plexuses during fetal development and hibernation
AU Oksche, A.; Kirschstein, H.; Vaupel-Von Harnack, M.
CS Univ. Giessen, Giessen, Fed. Rep. Ger.
SO Zeitschrift fuer Zellforschung und Mikroskopische Anatomie (1969), 94(2), 232-51 CODEN: ZZACAG; ISSN: 0044-3794
DT Journal
LA German
AB Choroidal epithelium of 3-4 month human fetuses and hibernating hedgehogs contains abundant glycogen. In epithelial cells of the human fetal choroid plexus, large masses of glycogen had displaced cytoplasmic organelles, such as numerous immature ***mitochondria*** and ***arrays*** of granular endoplasmic reticulum, to the cell apex or periphery. Mitochondria were also observed in the single cytoplasmic strands and the plexiform cytoplasmic differentiations that penetrated into glycogen masses. In choroidal epithelial cells of the hibernating hedgehog, numerous mitochondria with platelike and tubular cristae were present. Glycogen particles were scattered throughout the cell and at times were clustered into apical or basal aggregates. The particles occurred in close assocn. with mitochondria and cisternae of a granular endoplasmic reticulum. The electron microscopic appearance of glycogen in the choroidal epithelium of the hibernating hedgehog resembled that described in the frog (Paul, 1968). The functional significance of the morphological forms of choroidal glycogen

depots is discussed in relation to fetal development and with reference of hibernating mammals and lower cold-blooded vertebrates.

L26 ANSWER 150 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1970:10268 CAPLUS <<LOGINID::20080906>>
DN 72:10268
OREF 72:1847a,1850a
TI Electron-microscopic investigations on lipid storage in the kidney tubules of Drosophila melanogaster
AU Wessing, Armin; Eichelberg, Dieter
CS Justus Liebig-Univ., Giessen, Fed. Rep. Ger.
SO Zeitschrift fuer Zellforschung und Mikroskopische Anatomie (1969), 94(1), 129-46 CODEN: ZZACAG; ISSN: 0044-3794
DT Journal; General Review
LA German
AB A review. In the cells of the renal tubules (Malpighian tubules) of D. melanogaster lipids are stored in the same way as 3-hydroxykynurenine. These substances are found in dilatations of the endoplasmic reticulum. In later larval stages the lipid droplets gradually disappear. In these stages the lipid droplets are either closely assocd. with the ***mitochondria*** or are removed by concentric membrane ***arrays*** of the endoplasmic reticulum. The functional significance of these findings is discussed. 57 refs.

L26 ANSWER 151 OF 151 CAPLUS COPYRIGHT 2008 ACS on STN
AN 1964:443528 CAPLUS <<LOGINID::20080906>>
DN 61:43528
OREF 61:7591f-g
TI Degeneration of mitochondria in lead poisoning
AU Watrach, A. M.
CS Univ. of Illinois, Urbana
SO Journal of Ultrastructure Research (1964), 10(3-4), 177-81 CODEN: JULRA7; ISSN: 0022-5320
DT Journal
LA Unavailable
AB Electron microscopic studies of the liver of swine given 20-60 mg. Pb(OAc)2/lb./day in the feed for 3-6 months revealed the presence of fine, closely packed ***arrays*** of lamellar formations in ***mitochondria*** . The lamellae were 55-85 A. thick and 0.1-0.5 .mu. long. Mitochondria contg. such structures were usually enlarged and had only a few, short cristae. The presence of these changes was interpreted as a sign of mitochondrial malfunction and degeneration of a nonspecific nature.

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(FILE 'HOME' ENTERED AT 15:16:47 ON 06 SEP 2008)
FILE 'CAPLUS' ENTERED AT 15:17:05 ON 06 SEP 2008
L1 243828 S (ARRAY? OR MICROARRAY?)/BI,AB
L2 12 S MITOCHONDI?/BI,AB
L3 181246 S MITOCHONDRI?/BI,AB
L4 2169 S L1 AND L3
L5 1872 S L4 NOT 2008/PY
L6 1513 S L5 NOT 2007/PY
L7 1201 S L6 NOT 2006/PY
L8 930 S L7 NOT 2005/PY
L9 708 S L8 NOT 2004/PY
L10 438 S L9 AND (DNA# OR CDNA# OR RNA#)/BI,AB
L11 0 S (CAENORABDIS)/BI,AB
L12 0 S CEANORABDIS/BI,AB
L13 0 S CAENORHABDUS/BI,AB
L14 0 S CAENORABDUS/BI,AB
L15 14138 S CAENORHABDITIS/BI,AB
L16 17793 S ELEGANS/BI,AB
L17 21945 S NEMATODE#/BI,AB
L18 33916 S L15 OR L16 OR L17
L19 4 S L10 AND L18
L20 283 S ((ARRAY? OR MICROARRAY?)(5A)MITOCHONDRI?)/BI,AB
L21 423 S ((ARRAY? OR MICROARRAY?)(10A)MITOCHONDRI?)/BI,AB
L22 376 S L21 NOT 2008/PY
L23 304 S L22 NOT 2007/PY
L24 239 S L23 NOT 2006/PY
L25 190 S L24 NOT 2005/PY
L26 151 S L25 NOT 2004/PY
L27 248 S L20 NOT 2008/PY
L28 196 S L27 NOT 2007/PY
L29 155 S L28 NOT 2006/PY
L30 119 S L29 NOT 2005/PY
L31 91 S L30 NOT 2004/PY

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